Delaval, Jan

From:

Sent:

Gambel, Phillip Tuesday, April 02, 2002 9:15 AM Delaval, Jan exam answer 09 / 020393

To:

Subject:

jan

please perform a sequence and a sequence interference search for

ussn 09 / 020393

open and closed

amino acids 42-58 of SEQ ID NO: 3

thanx

phillip gambel art unit 1644 308-3997

Rcom 8303

1644 mailbox

please let me know when it is ready. thanx.

Jan Delaval Reference Librarian Biotechnology & Chemical Library CM1 1E07 - 703-308-4498 jan.delaval@uspto.gov



SEARCH REQUEST FORM

Scientific and Technical Information Center

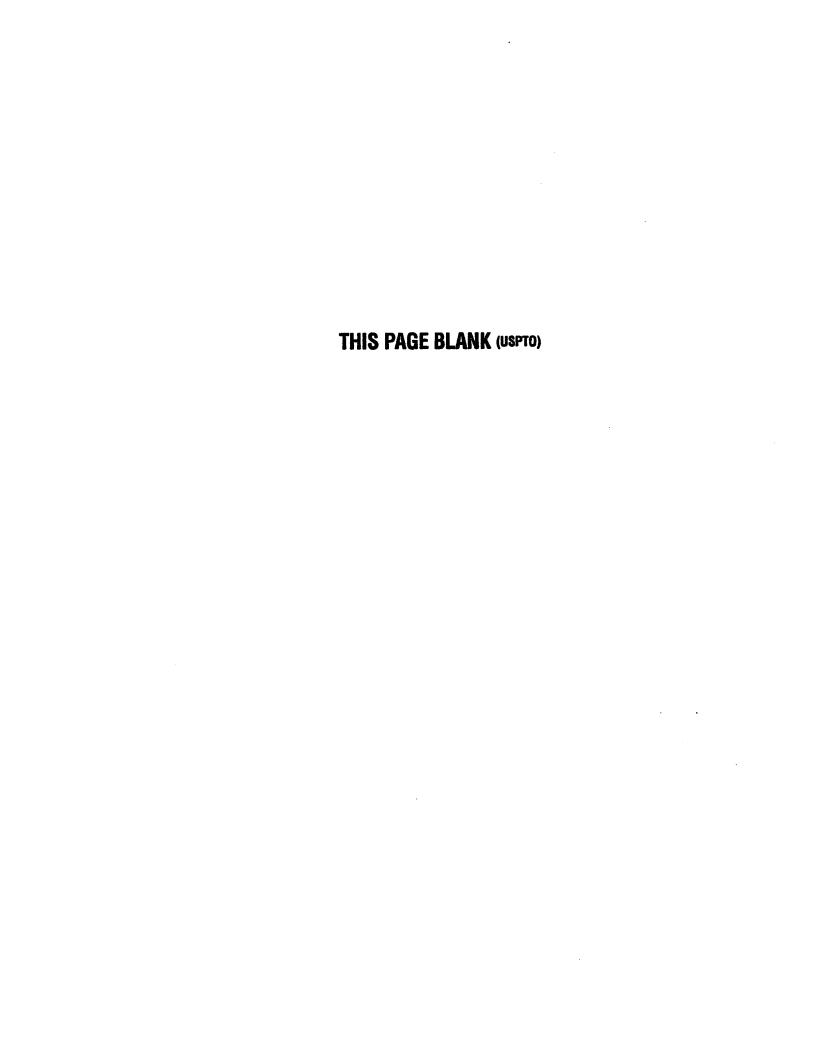
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Requester's Full Name:		Examiner # : Serial Number:	Date:
Art Unit:	Phone Number 30	Serial Number: _	
Mail Box and Bldg/Room	Location:	Results Format Preferred (ci	rcle): PAPER DISK E-MAII
If more than one search	is submitted, please	prioritize searches in order o	f need. **********
Please provide a detailed statem Include the elected species or str	ent of the search topic, and ructures, keywords, synony any terms that may have a s	describe as specifically as possible th ms, acronyms, and registry numbers, special meaning. Give examples or re	e subject matter to be searched. and combine with the concept or
Title of Invention:		er er	
Inventors (please provide full	names):	· · · ·	
 			
Earliest Priority Filing Dat			
For Sequence Searches Only Pl appropriate serial number.	lease include all pertinent info	ormation (parent, child, divisional, or iss	ued patent numbers) along with the
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		Віс	Jan Delaval. Reférence Librarian technology & Chemical Library CM1 1E07 – 703-308-4498 jan.delaval@uspto.gov
		<i>2</i> **	
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*******	******	*******	*******
STAFF USE ONLY	Type of Search	vendors and co	st where applicable
Searcher: an	NA Sequence (#)_	STN	
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Searcher Location:	Structure (#)	Questel/Orbit	
Date Searcher Picked Up: 4/2		Dr.Link	
Date Completed: 4/L	U Litigation	Lexis/Nexis	
Searcher Prep & Review Time:	Fulltext Family	Sequence Systems	

PTO-1590 (8-01)

W

Other

Other (specify)_



63548

Delaval, Jan

From:

Sent:

To: Subject:

Gambel, Phillip Tuesday, April 02, 2002 10:07 AM Delaval, Jan second sequence to search for 09 /020393

jan

please perform a sequence and a sequence interference search

both open and closed

for

09 / 020393

SEQ ID NO: 18

thanx

phillip gambel art unit 1644 308-3997

1644 mailbox 9E12

Jan Delaval. Reference Librarian Biotechnology & Chemical Library CM1 1E07 – 703-308-4498 jan.delaval@uspto.gov

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Minimum
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SUMMARIES

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50	49	48	47	46	45	44	43	42	41	40	39	38	37	36	ω 5	34	<u>ω</u>	32	31	30
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40.6	40.6	40.6			40.6	41.1	41.1	41.1	41.1	41.1	41.1	41.7	41.7	41.7	41.7	41.7	41.7	41.7	41.7	42.7
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ALIGNMENTS

A;Cross references: GB:M84349; GB:M82840; NID:g180149; PIDN:AAA88793.1; PID:g180151
A;Note: sequence extracted from NCBI backbone (NCBIN:112714, NCBIN:112718, NCBIN:1127
R;Davies, A.; Simmons, D.L.; Hale, G.; Harrison, R.A.; Tighe, H.; Lachmann, P.J.; Wal
J. Exp. Med. 170, 637-654, 1989
A;Title: CD59, an LY-6-like protein expressed in human lymphoid cells, regulates the A;Reference number: JL0109; MUID:89361238
A;Accession: JL0109 C;Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 08-Dec-2000 C;Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 08-Dec-2000 C;Accession: A46252; JL0109; A33405; JU0134; A34587; S05504; S09201; A60828; PL0041; R;Petranka, J.G.; Fleenor, D.E.; Sykes, K.; Kaufman, R.E.; Rosse, W.F. Proc. Natl. Acad. Sci. U.S.A. 89, 7876-7879, 1992 A;Title: Structure of the CD59-encoding gene: further evidence of a relationship to A;Reference number: A46252; MUID:92390353 surface glycoprotein CD59 precursor [validated] - human N;Alternate names: 1F5 antigen protein; 20K homologous restriction factor (HRF20); CD plex inhibition factor (MACIF); membrane inhibitor of reactive lysis (MIRL); protecti C;Species: Homo sapiens (man) A; Molecule type: DNA A; Residues: 1:128 < PET> A; Accession: A46252

A;Cross-references: EMBL:X16447; NID:g29805; PIDN:CAA34467.1; PID:g29806 R;Okada, H.; Nagami, Y.; Takahashi, K.; Okada, N.; Hideshima, T.; Takizawa, H.; Kondo Biochem. Biophys. Res. Commun. 162, 1553-1559, 1989 A;Title: 20 KDa homologous restriction factor of complement resembles T cell activati A;Reference number: A33405; MUID:89350983 A; Molecule type: mRNA A; Residues: 1-128 <DAV> A; Accession: A33405

A;Cross-references: GB:M27909; NID:g623406; PIDN:AAA60543.1; PID:g623407 R;Sugita, Y.; Tobe, T.; Oda, E.; Tomita, M.; Yasukawa, K.; Yamaji, N.; Takemoto, J. Biochem. 106, 555-557, 1989 A; Title: Molecular cloning and characterization of MACIF, A; Reference number: JU0134; MUID:90110046 A; Molecule type: mRNA A; Residues: 1-128 < OKA>

A; Accession: JU0134

A;Note: parts of this sequence, including the amino end of the mature protein, were c A;Note: Sites for glycosylation and the absence of glycosylation were confirmed R;Sawada, R; Chashi, K.; Anaguchi, H.; Okazaki, H.; Hattori, M.; Minato, N.; Naruto, DNA Cell Biol. 9, 213-220, 1990
A;Title: Isolation and expression of the full-length cDNA encoding CD59 antigen of hu A;Reference number: A34587; MUID:90253615 A; Molecule type: mRNA A; Residues: 1-128 <SUG>

an inhibitor of membrane

Ŧ.; c_b

A;Cross-references: GB:M34671; NID:9180152; PIDN:AAA51952.1; PID:9180153

A; Molecule type: mRNA A; Residues: 1-128 <SAW>

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A; Molecule type: protein
A; Residues: 26-42, 'XX', 45-50, 'X', 52, 'X', 54-57, 'X', 59-63 <HAR>
R; Ninomiya, H; Stewart, B.H.; Rollins, S.A.; Zhao, J.; Bothwell, A.L.M.; Sims, P.J.
A; Title: Contribution of the N-linked carbohydrate of erythrocyte antigen CD59 to its contribution of the N-linked carbohydrate of erythrocyte antigen CD59 to its contribution of the N-linked carbohydrate of erythrocyte antigen CD59 to its contribution of carbohydrate of erythrocyte antigen CD59 to its contribution of carbohydrate of erythrocyte antigen CD59 to its contribution of carbohydrate of erythrocyte antigen CD59 to its contribution of carbohydrate of erythrocyte antigen CD59 to its contribution of carbohydrate of erythrocyte antigen CD59 to its contribution of carbohydrate of erythrocyte antigen CD59 to its contribution of carbohydrate of erythrocyte antigen CD59 to its contribution of carbohydrate of carbohydrate of erythrocyte antigen CD59, A; Reference number: PX0068; MUID:94103166
A; Reference number: PX0068; MUID:94103166
A; Residues: 26-29:30-39:40-42, 'X', 44-48:49-52;56-65;65-72;88-90;92-96 <SU2>
A; Title: Gene structure of human CD59 and demonstration that discrete mRNAs are generate A; Carbohydrate of human CD59 and demonstration that discrete mRNAs are generate A; Carbohydrate of human CD59 and demonstration that discrete mRNAs are generate A; Carbohydrate of human CD59 and demonstration that discrete mRNAs are generate A; Carbohydrate of human CD59 and demonstration that discrete mRNAs are generate A; Carbohydrate of human CD59 and demonstration that discrete mRNAs are generate A; Carbohydrate of human CD59 and demonstration that discrete mRNAs are generate A; Carbohydrate of human CD59 and demonstration that discrete mRNAs are generate A; Carbohydrate of human CD59 and demonstration that discrete mRNAs are generate A; Carbohydrate of human CD59 and demonstration that discrete mRNAs are generate A; Carbohydrate of human CD59 and demonstration discrete mRNAs are generate CD50 and CD50 and CD50 and CD50 and CD50 
A;Cross-references: EMBL:214113; NID:g29810; PIDN:CAA78486.1; PID:g825637 C;Comment: This cell surface antigenic glycoprotein inhibits homologous complement 1 C;Comment: This glycosylphosphatidylinositol-anchored protein is deficient in cases A;Gene: GDB:CD59
A.;Coross-references: GDB:119769; OMIM:107271
                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-128 < RES>
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A;Rosidues: 26-42 <STE>
R;Harada, R; Okada, N; Fujita, T.; Okada, H.
J. Immunol. 144, 1823-1828, 1990
A;Ritle: Purification of 1F5 antigen that prevents complement attack on homologous cell
A;Accession: A60774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Experimental source: normal urine
A;Note: the six unknown or mismatched residues in the amino-terminal fragment correspond
R;Stefanova, I, Hilgert, I, Kristofova, H, Brown, R.; Low, M.G.; Horejsi, V.
Mol. Immunol. 26, 153-161, 1989
A;Title: Characterization of a broadly expressed human leucocyte surface antigen MEM.
A;Accession: PL0041; MUID:89143489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Residues: 26-27,'V',29-30,'D',32-37,'X',39-42,'XX',45-50,'X',52-62;'VXRLID'
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R;Cabral, A.R.; Cole, L.A.; Walz, D.A.; Castor, C.W.
Arthritis Rheum. 30, 1393-1400, 1987
A;Title: Connective tissue activation. XXXII. Structural and biologic characteristics of A;Accession: A60828; MUID:88134429
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A;Residues: 27-128 <SA2>
A;Cross-references: EMBL:X15861; NID:g29803; PIDN:CAA33870.1; PID:g1340180
R;Philbrick, W.M.; Palfree, R.G.E.; Maher, S.E.; Bridgett, M.M.; Sirlin, S.; Bothwell, Eur. J. Immunol. 20, 87-92, 1990
A;Title: The CD59 antigen is a structural homologue of murine Ly-6 antigens but lacks A;Accession: S09201; MUID:90168959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Complementary DNA sequence and deduced peptide sequence for CD59/MEM-43
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                                                                                                                                                                           of
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A;Cross references: GB:L22863; NID:g514314; C;Superfamily: Ly-6 antigen; Ly-6 homology F;26-102/Domain: Ly-6 homology <LY6>
                                                                 A; Molecule type: DNA
A; Residues: 1-128 < RES>
                                                                                   A:Status: preliminary: translated from GB/EMBL/DDBJ
                                                                                                                      A;Reference number: I36894;
A;Accession: I36894
                                                                                                                                          R:FOGOr, W.L.; Rollins, S.A.; Bianco-Caron, S.; Burton, W.V.; Guilmette, A;Title: Primate terminal complement inhibitor homologues of human once
                                                                                                                                                                                                                C)Species: Cercopitheous aethiops (green monkey, grivet)
C)Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text,
C)Accession: 136894
                                                                                                                                                                                                  R; Fodor, W.L.;
                                                                                                                                                                                                                                                                     CD59 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:L22862; NID:g514327; C;Superfamily: Ly-6 antigen; Ly-6 homology F;26-100/Domain: Ly-6 homology <LY6>
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A;Aecession: 136914
A;Aecession: 136914
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C;Species: Papio sp. (baboon)
C;Date: 07-Jun-1996 #text_change 23-Jul-1999
C;Accession: I36914 #sequence_revision 07-Jun-1996 #text_change 23-Jul-1999
T;Podor, W.L.; Rollins, S.A. Biccare
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A;Note: the first intron occurs before the initiator codon
C;Superfamily: Ly-6 antigen; Ly-6 homology
C;Keywords: blocked carboxyl end; glycoprotein; lipoprotein; membrane protein; phosph
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-102/product: surface glycoprotein CD59 #status experimental <MAT>
F;26-102/pomain: Ly-6 homology <LYGS
F;103-128/Domain: Cy-6 homology <LYGS
F;28-51.31-38/44-64/Disulfide bonds: #status experimental
F;28-51.31-38/44-64/Disulfide bonds: #status experimental
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Query Match Best Local Similarity

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. 68;

Score Pred.

63; No.

DB 2; 0.0042;

Length 128;

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hypothetical protein F11C1.5b - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T20767
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T20767
probable transcription regulator PA0708 [imported] - Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
                                                 RESULT
E83557
                                                                                                                                                              Query Match
Best Local Similarity
Watches 12; Conserv.
                                                                                                                                                                                                                                                           A; Map position: X
A; Introns: 21/1; 97/3;
9/3; 1659/3; 1700/2
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C; Species: Caenorhabditis elegans
C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #te
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A; Residues: 1-1302 <WIL>
A; Cross-references: EMBL: Z54270;
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A; Residues: 1-1767 <WIL>
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Pred. No. 31
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Pred. No. 22;
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A; Experimental source: C; Genetics: A; Gene: CESP: F23A7.5 A; Map position: X
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A; Gene:
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Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic A;Reference number: A82950; MUID:20437337
A;Accession: E83557
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R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; M1
R;Stover, C.K.; Pham, Y.; Brody, L.L.; Coulter,
                                                                      A;Status: preliminary; translated A;Molecule type: DNA A;Residues: 1-1307 <WILL A;Cross-references: EMBL:Z81067; F
                                                                                                                                                                                                   C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999
C;Accession: 721283
R;McMurray, A.
                                                                                                                                               A; Reference number: A; Accession: T21283
                                                                                                                                                              submitted to the EMBL Data Library, October 1996
A;Reference number: Z19401
                                                                                                                                                                                                                                                          hypothetical protein F23A7.5 - Caenorhabditis elegans C; Species: Caenorhabditis elegans
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A;Molecule type: DNA
A;Residues: 1-777 <STO>
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A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans
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A; Residues: 1-284 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:AP001509; GB:BA000004; NID:g10173176; PIDN:BAB04508.1; GSPDB:GA;Experimental source: strain C-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000
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                                                                          EMBL: Z81067; PIDN: CAB02976.1; GSPDB: GN00028; CESP: F23A7.5
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46.78;
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ed. No. 16;
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r, S.N.; Folger, F
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Дb
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A;Start codon: TTG
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                                                                                                                                                                                                                                                                                                      A;Reference number: A69000; MUID:98037514
A;Accession: D69102
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-807 <MTH>
                                                                                                                                                                                                                                                                                                                                                                                                                                      collagenase - Methanobacterium thermoautotrophicum (strain Delta H)
C;Species: Methanobacterium thermoautotrophicum
C;Decession: D69102
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, ; Olu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A.mitto. Commondate.
                                                                                                                        Query Match
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D69102
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A;Molecule type; DNA
A;Residues: 1-205 <AND>
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A;Accession: H71639
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R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C:Species: Rickettsia prowazekii
C:Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 03-Nov-2000
                                        J 1 FEHCNFNDVTTRLRE 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) I chain J RP790 - Rickettsia prowazekii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
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               562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77 NENQAITKLREN 88
  FRECOWNDVRSILRE 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 NENDVTTRLREN 16
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les 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           654 CKINDDTTILREN 666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 CNFNDVTTRLREN 16
                                                                                                   Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 69.2
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                              45.8%;
53.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46.98;
69.28;
                                                                                                      Score 44;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 44; DB
Pred. No. 8.3;
1; Mismatches
                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 45; DB 2;
Pred. No. 39;
0; Mismatches 4
                                                                                                      35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB
8.3;
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oxidoreductase
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                                                                                                                   Length 807
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jiwani,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0,
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RESULT
C83681
                                                                                                                                  Query Match
Best Local Similarity 56.20
"Checkes 9; Conservative
                                                                                              В
                                                                                                                                       Qy
                                                                                                                                                                                                                                                                                    A:Map position: 5
A:Introns: 93/2; 104/1; 298/3
                                                                                                                                                                                                                                                                                                                                            A; Gene: CESP:Y102A5C.1
                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-365 <WI2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Experimental source: clone F09C6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-365 <WIL>
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Best Local Similarity 75.0
"~+~hes 6; Conservative
                                                                       288 FEHLCFQDVKERLLES 303
                                                                                                                     1 FEHCNFNDVTTRLREN 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 HCNFTDIT 108
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75.0%;
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ABC transporter (substrate-binding protein) BH0251 [imported] - C;Species: Bacillus halodurans
                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:AL031627; PIDN:CAA20972.1; CESP:Y102A5C.
A;Experimental source: clone Y102A5C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R:Gardner, A.
submitted to the EMBL Data Library, September 1998
A:Reference number: Z20204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:281496; PIDN:CAB04075.1; GSPDB:GN00023; CESP:Y102A5C.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, November 1996
A;Reference number: 219305
A;Accession: T20652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein Y102A5C.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C;Accession: T20652; T26370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-544 <CAV>
A; Cross-references: EMBL: X64737; NID: g453158;
A; Note: the nucleotide sequence was submitted
C; Superfamily: coronavirus EZ glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arch. Virol. 130, 471-476, 1992
A; Title: Sequence analysis of strains of avian infectious bronchitis coronavirus 1sol
A; Reference number: $41626
A; Accession: $41626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       spike protein chain 1 precursor - avian infectious bronchitis virus (fragment) c;Species: avian infectious bronchitis virus, IBV c;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Sep-1999 c;Accession: S41626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                Score 42; DB;
Pred. No. 32;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 43; DB
Pred. No. 33;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     GB/EMBL/DDBJ
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                                                                                                                                                                                                                                 Length 365,
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    Bacillus halodurans
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Library, March 1992
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hypothetical protein yqzD - Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 28-Jul-2000
C;Accession: C69969
C; Accession: C69969
R;Kunst, F:; Ogasawara, N.; Moszer, I:; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter, C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd
A; Ebrilich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
A;Authors: Fooliger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueelly, M.; Gydwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A.;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serorakeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein T19C3.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T16889
R:Fulton, L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Description: The sequence of C. elegans cosmid T1:
A;Reference number: Z18598
A;Accession: T16889
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-464 <FUL>
A;Cross-references: EMBL:U28412; NID:9849235; PID:91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data Library, June 1995 A; Description: The sequence of C. elegans cost A; Reference number: Z18598
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A; Residues: 1-419 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               В
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Matches
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Accession: C83681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  108 HAKFTEVITRLKKN 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 HCNFNDVTTRLRENE 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HCNFNDVTTRLREN 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL:U28412; NID:g849235; PID:g849239; PIDN:AAC46596.1; CESP:T19C3.
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Pred. No. 41;
3; Mismatches
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H+-transporting ATP synthase (EC 3.6.1.34) chain b - Odontella sinensis chloroplast N;Alternate names: ATP synthase CF0 chain I; H+-transporting ATP synthase chain I C;Species: chloroplast Odontella sinensis C;Date: 03-May-1994 #sequence_revision 20-Feb-1995 #text_change 20-Jun-2000 C;Accession: S23358; S14444; S78819 R;Pancic, P.G.; Strotmann, H.; Kowallik, K.V. J. Mol. Biol. 224, 529-536, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T: Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A. A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus A;Reference number: A69580; MUID:98044033
A;Accession: C69969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Chloroplast ATPase genes in the diatom A;Reference number: S21682; MUID:92219274 A;Accession: S23358
                                                                                                                      A;Genome: chloroplast
C;Superfamily: H+-transporting ATP synthase chain I
C;Keywords: ATP biosynthesis; chloroplast; hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                             A;Note: this ORF is not annotated in GenBank entry PLOSATPD, release 109.0 R;Kowallik, K.V.; Stoebe, B.; Schaffran, I.; Kroth-Pancic, P.; Freier, U. Plant Mol. Biol. Rep. 13, 336-342, 1995
A;Title: The Chloroplast Genome of a chlorophyll a+c- containing Alga, Odontella sine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Title: The delta subunit of the chloroplast ATPase A; Reference number: S14323; MUID:91192176 A; Accession: S14444
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A;Cross-references: EMBL:X60752; NID:g11937; PIDN:CAA43162.1; PID:g11942
R;Pancic, P.G.; Strotmann, H.; Kowallik, K.V.
FEBS Lett. 280, 387-392, 1991
                                                                                                                                                                                                                                                    A;Cross-references: EMBL:267753; NID:g1185127; PIDN:CAA91692.1; PID:g1185209
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1995
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A; Residues: 1-17
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C;Superfamily:
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A; Residues: 1-117 < KUN>
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                                                                                                                                                                                                                                                                                                                                                                             A; Accession:
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A; Residues: 141-179 < PAN2>
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Best Local
  Local Similarity
les 8; Conserv
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                                                                                                                                                                                                                                                                                                      1-179 <KOW>
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                          42.7%;
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43.8%;
Score 41; DB Pred. No. 22; 1; Mismatches
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Pred. No.
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5 NFNDVTTRLRENE

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NFNQIFTLLAENE

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related to integral membrane protein pth11 [imported] - Neurospora crassa C;Species: Neurospora crassa C;Species: Neurospora crassa C;Date: 28.Jul.-2000 #sequence_revision 28.Jul.-2000 #text_change 28.Jul.-2000 R;Schulte, U; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; submitted to the Protein Sequence Database, July 2000
                                                                                                                                                                   RESULT 19
T51212
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                                                                                                                                                                                                                                                                Qy
                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-265 <MES>
A;Cross-references: EMBL:273274; NID:g1360485; PIDN:CAA97667.1; PID:g1360486; GSPDB:GNOC
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                          A; Map position: 12R
C; Superfamily: Saccl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to the Protein Sequence Database A. Accession: S64938
A. Molecula *---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein YLR102c - yeast (Saccharomyces cerevisiae) N;Alternate names: hypothetical protein L2710 C.Species: Saccharomyces cerevisiae C.Date: 01-Aug-1995 #sequence_revisiae C.Accession: S64938 #sequence_revision 24-May-1996 #text_change R.Messenguy, F.; Dubois, E.; Vierendeels, F.; Scherens, B. submitted to the Protein Sequence Database, May 1996
                                                                                                                                                                                                                                                                                                  Matches
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C:Superfamily: tobacco rattle virus coat protein
C:Keywords: coat protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:X03241,
A;Note: the authors translated
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Bergh, S.T.; Koziel, M.G.; Huang, S.C.; Thomas, R.A.; Gilley, D.P.; Siegel, Nucleic Acids Res. 13, 8507-8518, 1985
A;Title: The nucleotide sequence of tobacco rattle virus RNA-2 (CAM strain).
A;Reference number: A26027; MUID:86093657
A;Accession: A26027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: genomic RNA
A; Residues: 1-223 <BER>
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Best Local
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                                                                                                                                                                                                                                                                                       Local Similarity 53.
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                                                                                                                                                                                                                                                                                                     42.78;
53.38;
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80.0%;
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Pred. No. 33;
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Pred. No. 28;
1; Mismatches
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A;Gene: CESP:K02B7.1
A;Map position: 2
A;Introns: 31/1; 196/2; 281/2; 357/3;
C;Superfamily: Caenorhabditis elegans
                                                                            A:Experimental source: clone K02B7 C;Genetics:
                                                                                                         A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-742 <WIL>
                                                                                                                                                                                                               hypothetical protein K02B7.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #Sequence_revision 15-Oct-1999 #text_change C;Accession: T23226
                                                                                                                                                                   A;Reference number:
A;Accession: T23226
                                                                                                                                                                                  submitted to the EMBL Data A; Reference number: Z19711
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T23226
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A; Introns: 45/1; 2
C; Superfamily: Sch
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A;Experimental source: strain 972h-; cosmid c32A11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Skelton, J.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V. submitted to the EMBL Data Library, February 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-720 <SKE>
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A; Accession: T38647
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Best Local S
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T38647
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A; Introns: 77/3; 251/2
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A,Status: preliminary
A;Molecule type: DNA
A;Residues: 1-410 < SCH>
A;Cross-references: EMBL:AL390354; GSPDB:GN00116; NCSP:B24M22.80
C;Genetics:
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Best Local S
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6; Conservative
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42.9%;
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Pred. No.
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Pred. No. 53;
4; Mismatches
393/1; 429/3; 474/2; hypothetical protein
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                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
95;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 720;
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           496/3; 546/2
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A;Status: pression A;Status: pression A;Rosidues: 1-281, 'H',283-805 <MAG>
A;Rosidues: 1-281, 'H',283-805 <MAG>
A;Rosidues: 1-281, 'H',283-805 <MAG>
A;Rosidues: EMBL:AF025465; PIDN:AAB71023.1; GA;Cross-references: EMBL:AF025465; PIDN:AAB71023.1; GA;Experimental source: strain Bristol N2; clone K02E7
R;Pauley, A.; Scheet, P.; Harper, M.
Submitted to the EMBL Data Library, February 1999
A;Description: The sequence of C. elegans cosmid W03
A;Description: The sequence of C. elegans cosmid W03
A;Description: The sequence of C. elegans cosmid W03
                                                       disease resistance protein RPP8 [validated] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 21-Jul-2000
C:Accession: T48898
R:McDowell, J.M.; Dhandaydham, M.; Long, T.A.; Aarts, M.G.; Goff, S.; Holub
Plant Cell 10, 1861-1874, 1998
A;Title: Intragenic recombination and diversifying selection contribute to the evolution A;Reference number: Z24999; MUID:99030193
A;Accession: T48898
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                                                                                                                                                                              T48898
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C; Superfamily: Caenorhabditis elegans hypothetical protein W03G1.4
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Best Local S
Matches
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Best Local
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Introns: 31/1
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8; Conserv
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8; Conser
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61.
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tol N2; clone W03G1
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                                                                              Goff, S.; Holub,
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A; Molecule type: DNA
A; Residues: I -1162 <NIE>
A; Cross-references: EMBL: M21883; NID: g331183;
C; Superfamily: Coronavirus E2 glycoprotein
C; Keywords: glycoprotein
                                                                                                                                                                                                                   E2 glycoprotein precursor - avian infectious bronchitis virus %; Alternate names: pepiomer glycoprotein N; Contains: E2 glycoprotein subunit S1; E2 glycoprotein subunit C; Species: avian infectious bronchitis virus, IBV C; Date: 18-Feb-1994 #sequence_revision 01-Dec-1995 #text_change
                                                                                                                           R:Niesters, H.G.M.; Lenstra, J.A.; Spaan, virus Res. 5, 253-263, 1986 A;Title: The peplomer protein sequence of A;Reference number: S07421; MUID:87021475
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A; Accession: T48899
                                                                                          A; Status: preliminary
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A; Introns: 2
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A;Cross-references: EMBL:AF089710; NID:g3928861; PIDN:AAC83165.1; PID:g3928862
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Pred. No. 1.2e+02;
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ALIGNMENTS

SMP3_YEAST ATF2_YEAST YMW5_YEAST PURL_CORAM

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Med. 170:637-654(1989).

Davies A., Simmons D.L., Hale G., Harrison R.A., Lachmann P.J., Waldmann H.;
"CD59, an LY-6-like protein expressed in human l regulates the action of the complement membrane homologous cells.";

human lymphoid cells,

attack complex on

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SEQUENCE FROM N.A. NCBI_TaxID=9606;

TISSUE-T-cell

MEDLINE=89361238; PubMed=2475570;

MEDLINE=90168959; PubMed=1689664; Philbrick W.M., Palfree R.G.E., Rog Bridgett M.M., Sirlin S., Bothwell

Roger G.E., Maher

s . E

of murine Ly-6 antigens

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"The CD59 antigen is a structural homologue but lacks interferon inducibility."; Eur. J. Immunol. 20:87-92(1990).

Biochem.
[4]

J.

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MEDITURE-90110046; PubMed-2606909;

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Sugita Y., Tobe T., Oda E., Tomita M., Yasukawa K., Yamaji N.,

Takemoto T., Furuichi K., Takayama M., Yano S.;

"Molecular cloning and characterization of MACIF, an inhibitor

membrane channel formation of complement.";

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Takizawa H., Kondo ..,
Takizawa H., Kondo ..,
Takizawa H., Kondo ..,
"20 KDa homologous restriction
activating protein.";
activating protein.";
Res. Commun.

162:1553-1559(1989)

factor of complement resembles

T cell

MEDLINE=89350983; Pubm Okada H., Nagami Y., T Takizawa H., Kondo J.;

PubMed=2475111;
v Takahashi K.,

Okada

Z

Hideshima

SEQUENCE FROM N.A.

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CD59_HUMAN STANDARL,

ID CD59_HUMAN STANDARL,

AC P13987;

AC P13987;

DT 01-JAN-1990 (Rel. 13, Created)

DT 01-JAN-1990 (Rel. 13, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE CD59 GLYCOPROTEIN PRECURSOR (MEMBRANE ATTACK COMPLEX INHIBITION

DE FACTOR) (MACIF) (MAC-INHIBITORY PROTEIN) (MAC-IP) (MEM43 ANTIGEN)

DE (PROTECTIN) (MEMBRANE INHIBITORY OF REACTIVE LYSIS) (MIRL) (20 KDA

"MONOLOGOUS RESTRICTION FACTOR) (HRF-20) (HFF20) (1F5 ANTIGEN).

"""""nidae; Homo.

"Isolation and expression of the full-length antigen of human lymphocytes.", DNA Cell Biol. 9:213-220(1990).

Sawada R., Ohashi K., SEQUENCE FROM N.A. MEDLINE=90253615; !

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sugita Y., Nakano Y., Oda E., Noda K., Tobe T., Miura N.H., Tomita "Petermination of carboxyl-terminal residue and disulfide bonds of MACIF (CD59), a glycosyl-phosphatidylinositol-anchored membrane
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SEQUENCE OF 27-128 FROM N.A.
MEDLINE-89386002; PubMed=2476718;
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"Complementary DNA sequence and deduced peptide sequence for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIINE-93021133; PubMed-1383553;
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"Gene structure of human CD59 and demonstration that discrete mrnas are generated by alternative polyadenylation.";
J., Mol. Biol. 227:971-976(1992).
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MEDILINE-92390353; PubMed=1381503;
Petranka J.G., Fleenor D.E., Sykes K., Kaufman R.E., Rosse W
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relationship to murine lymphocyte antigen Ly-6 protein.";
Proc. Natl. Acad. Sci. U.S.A. 89:7876-7879(1992).
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D59 responsible (
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EMBL; X17198; CAA35055 9;
EMBL; X17198; CAA33870 1;
EMBL; M34671; AAA51952 1;
EMBL; M34671; AAA51952 1;
EMBL; M43445; NOT_ANNOTATED_CDS.
EMBL; M4349; AAA88793 1; JOINED.
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EMBL; Z14116; CAA78486 1; JOINED.
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RT FETUCTURE Of a SOLUBLe, 91.VOSYLATED FOR THE human complement of a SOLUBLE, 91.
RT regulatory protein CD59."
RI Structure 2:185-199(1994).
CC COMPLEX (MAC) ACTION. ACTS BY BINDING TO THE C8 AND/OR C9
CC COMPLEX (MAC) ACTION. ACTS BY BINDING TO THE C8 AND/OR C9
CC COMPLEXENTS OF THE ASSEMBLING MAC, THEREBY REVERTING
CC COMPLEXED TO A PROTEIN THIS INHIBITOR APPEARS TO BE
ACTIVATION OF THE OSMOLYTIC PORE. THIS INHIBITOR APPEARS TO BE
ACTIVATION COMPLEXED TO A PROTEIN TYROSINE KINASE. INTERACTS WITH
CC T-CELL SURFACE ANTICEN CD2.
CC I- FUM: N-AND O-CLYCOSYLATED. THE N-GYCOSYLATION MAINLY CONSISTS OF A LACTOSAMINE EXTENSIONS AND OUTER ARM FUCOSE RESIDUES. THE
CC I- FUM: N-AND O-CLYCOSYLATED. THE N-GYCOSYLATED ROWS MITH AND WITHOUT
CC LACTOSAMINE EXTENSIONS AND OUTER ARM FUCOSE RESIDUES. THE
CC ARE PROBABLY ON THR-76 AND THE-77.
CC ARE PROBABLY ON THR-76 AND THR-77.
CC AT MINIMAL LEVELS IN NONDIABETIC SUBJECTS, BUT ONLY
CC MAC-INHIBITORY FUNCTION AND CONFERS TO VASCULAR COMPLICATIONS OF
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SIMILARITY: CONTAINS 1 UPAR/LY6 DOMAIN.
DATABASE: NAME-PROW; NOTE=CD guide CD59 entry;
WWW-"http://www.nobi.nlm.nih.gov/prow/cd/cd59.htm".
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MEDLINE=94103166;

AND DISULFIDE BONDS

PubMed=8276756;

Nucleic Acids Res. 17:6728-6728(1989).

SEQUENCE FROM N.A.

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Biol. Chem.

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OF.

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"Mutational analysis of the active site a
complement-inhibitory glycoprotein, CD59.

Exp. Med. 185:507-516(1897).

Rushmere

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Q1-NOV-1997 (Rel. 35, Last annotation update)
Q1-NOV-1997 (Rel. 35, Last annotation update)
CD59 GLYCOPROTEIN PRECURSOR (MEMBRANE ATTACK COMPLEX INHIBITION CD59 GLYCOPROTEIN) (MAC-IP) (PROTECTIN).
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-1- FUNCTION: POTENT INHIBITOR OF THE CCOMPLEX (MAC) ACTION. ACTS AT OR AF
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Catarrhini; Cercopithecidae;
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-i- FUNCTION: POTENT INHIBITOR OF THE COMPLEMENT MEMBRANE ATTACK COMPLEX (MAC) ACTION. ACTS AT OR AFTER THE C5B-8 STAGE OF MAC
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Mammalia; Eutheria; Primates; Catarrhini;
Cercopithecinae; Cercopithecus.
                                                                                                                                                                                                                                                                                                                                                                               (BY SIMILARITY).
-!- SIMILARITY: CONTAINS 1 UPAR/LY6 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=95104908; PubMed=7528724; Fodor W.L., Rollins S.A., Bianco-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cercopithecus aethiops (Green
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CD59.
                                                         SEQUENCE
                                                                                                                                        DOMAIN
                                                                                                                                                                        CHAIN
                                                                                                                                                                                                          PROSITE;
                                                                                                                                                                                                                      SMART; SM00134; LU;
                                                                                                                                                                                                                              Pfam; PF00021; UPAR_LY6;
                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9534;
                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 FEHCNFNDVTTRLRENE
                                                                                                                                                                                                                                                                                                                                                                                                                   ASSEMBLY
                                                                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FANCNFNDISTLLKESE
           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                              Glycoprotein;
                                                                                                                                                                                                          PS00983; LY6_UPAR;
                                                                                                                                                                                                                                                                                                                                              the Swiss Institute of Bioinformatics
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103
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58.8%;
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                                                                                                                                                                                               GPI-anchor;
             . 88;
                                                         MW.
                                                        BY SIMILARITY.
OF CHORD GLCNAC.
W: 9778DEEF7F7F05152 C
 Pred. No. 0.0
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score
Pred.
                                                                                                                                               CD59 GLYCOPROTEIN.
REMOVED IN MATURE FORM (BY GPI-ANCHOR (BY SIMILARITY)
                       Score 63;
                                                                                                                                        UPAR/LY6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   monkey) (Grivet).
Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     otation update)
EMBRANE ATTACK C
Y PROTEIN) (MAC-
                                                                                                                                                                                    SIMILARITY
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                                                                                                                                                                                                                                                                                                                Usage
                                                                                                                                                           FORM (BY SIMILARITY).
                       Length 128
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                                                          CRC64;
                                                                                                                                                                                                                                                                                                                                                 and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PROTECTIN)
                                                                                                                                                                                                                                                                                                                                                                                                         BY A GPI-ANCHOR
                                                                                                                                                                                                                                                                                                               bу
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                                                                    (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                     restrictions
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                                                                                                                                                                                                                                                                         Antigen;
                                                                                                                                                                                                                                                                                  SMART; SM00134; LU;
PROSITE; PS00983; L;
                                                                                                                                                                                                                                                                                                InterPro; IPR001526; LY6_UPAR.
Pfam; PF00021; UPAR_LY6; 1.
                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                       1 FEHCNFNDVTTRLREN 16
                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-98221206; PubMed-9553129;
Zhao X.-J. Zhao J., Zhou Q., Sims P.J.;
Tidentity of the residues responsible for the species-restricted
J. Biol. Chem. 273:10665-10671 (1998).

I. FUNCTION: POTENT INHIBITOR OF THE COMPLEMENT MEMBRANE ATTACK
COMPLEX (MAC) ACTION. ACTS BY BINDING TO THE C8 AND/OR C9
INCORPORATION OF THE MILITIPLE COPIES OF C9 REQUIRED FOR COMPLETE
FORMATION OF THE MILITIPLE COPIES OF C9 REQUIRED FOR COMPLETE
FORMATION OF THE OSMOLYTIC PORE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CD59_RABIT STANDARD; PKT; 127....
077541;
077541;
20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
CD59 GLYCOPROTEIN PRECURSOR (MEMBRANE ATTACK COMPLEX INHIBITION
CD59_CTCOPROTEIN PROTEIN) (MAC-IP) (PROTECTIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Lymphocytes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: CONTAINS 1 UPAR/LY6 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MISCELLANEOUS: THE MATURE FORM OF THIS CD59 CONTAINS AN ADDITIONAL SERINE RESIDUE BEFORE THE CONSERVED N-TERMINAL LEUCINE RESIDUE FOUND IN ALL OTHER CD59 HOMOLOGS SEQUENCED TO DATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPT-ANCHOR
                                                                Similarity
                                                                                                                                                                                                                                                                  Glycoprotein;
                                                Conservative
                                                                                                          101
13870 MW;
                                                                                                                                                                                                                                                                         LY6_UPAR; FALSE_NEG
                                                                                                                                          101
124
101
51
38
64
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94
                                                         51.0%;
50.0%;
                                                                                                                                                                                                                                                         GPI-anchor; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AND SEQUENCE OF 25-64.
                                      Score 49; DB 1;
Pred. No. 0.21;
3; Mismatches
                                                                                                                                          UPAR/LY6

UPAR/LY6

BY SIMILARITY

BY SIMILARITY

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BY SIMILARITY
                                                                                               N-LINKED (GLCNAC. . .) (POT GPI-ANCHOR (BY SIMILARITY).; CEA64C816772CABD CRC64;
                                                                                                                                                                                                         CD59 GLYCOPROTEIN.
REMOVED IN MATURE FORM (BY SIMILARITY).
                                                               <u>,</u> _,
                                      5
                                                           Length 124;
                                     Indels
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RESULT
CD59_CA
ID CC
AC P4
DT 01
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CD59_AOTTR
AC P51447
DT 01-OCT
DT 01-
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                                                                                                                                                                                                                                 Matches
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Best Local
67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM use by non-profit institutions as long as its content entities requires a license agreement (See http://www.isb-s
                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L22861; AAA35372.1; -. HSSP; P13987; 1CDQ.
                                                                                                                                                                          1 FEHCNFNDVTTRLRENE 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FOGOT W.L., ROLLINS S.A., Bianco-Caron S., Burton W.V., Guilmette E.R., Rother R.P., Zavoico G.B., Squinto S.P., "Primate terminal complement inhibitor homologues of human CD59.", Immunogenetics 41:51-51(1995).

-i- FUNCTION: POTENT INHIBITOR OF THE COMPLEMENT MEMBRANE ATTACK COMPLEX (MAC) ACTION. ACTS AT OR AFTER THE C5B-8 STAGE OF MAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: CONTAINS 1 UPAR/LY6 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE=95104908;
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P51447;
P51447;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
CD59 GLYCOPROTEIN PRECURSOR (MEMBRANE ATTACK COMPLEX INHIBITION FACTOR) (MACCIF) (MAC-INHIBITORY PROTEIN) (MAC-IP) (PROTECTIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aotus trivirgatus (Night monkey) (Douroucouli),
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
                                                                                                                                         FEDCTFSRVSNQLSENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ASSEMBLY.
SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR
                                                                                                                                                                                                                            Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SM00134; LU;
E; PS00983; L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycoprotein;
1 25
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                                                                                                                                                                                                                                   51.0%;
52.9%;
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                                                                                                                                                                                                                                             PubMed=7528724;
                                                                                                                                           83
                                                                                                                                                                                                        Score 49; DB
Pred. No. 0.22
3; Mismatches
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                                       PRT;
                                                                                                                                                                                                                            DB 1
0.22;
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.B., Squinto S.P.;
homologues of human CD59.";
                                                                                                                                                                                                          5,
                                                                                                                                                                                                                                         Length 128,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              FORM (BY SIMILARITY).
                                                                                                                                                                                                      Indels
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FOODOR W.L., Rollins S.A., Bianco-Caron S., Burton W.V., Guilmette E.R., Rother R.P., Zavoico G.B., Squinto S.P., "Primate terminal complement inhibitor homologues of human Immunogenetics 41:51-51(1995).

-I- FUNCTION: POTENT INHIBITOR OF THE COMPLEMENT MEMBRANE AT COMPLEX (MAC) ACTION. ACTS AT OR AFTER THE C5B-8 STAGE OF ASSEMBLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
CD59 GLYCOPROTEIN PRECURSOR (MEMBRANE ATTACK COMPLEX INHIBITION
CD59 GLYCOPROTEIN (MAC-INHIBITORY PROTEIN) (MAC-IP) (PROTECTIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This
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                                 HYPOTHETICAL
T19C3.5.
                                                                                                                                       YSV5
                                                                                                                                                        CAEEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00021; UPAR_LY6; SMART; SM00134; LU: 1
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Mammalia; Eutheria;
                 Caenorhabditis elegans
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 Eukaryota;
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1-NOV-1997
1-NOV-1997
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sen the Swiss Institute of Bioinformatics and the EN
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8; Conserv
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Metazoa;
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(Rel.
(Rel.
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                                                                                                                                       STANDARD;
                                                 35, Created)
35, Last sequence and KDA PROTEIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=7528724;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LY6_UPAR;
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Primates;
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47.1%;
Nematoda;
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                                                 Last sequence update)
Last annotation update)
PROTEIN T19C3.5 IN CHRO
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Platyrrhini;
Chromadorea; Rhabditida;
                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                        Mismatches
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KOWALIIK K.V., Stoebe B., Sch
"The chloroplast genome of a
Odontella sinensis.";
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SIGNAL 1 17 POTENTIAL.
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SMART; SM00329; BPI2; 1
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MEDLINE=92219274; PubMed=1532839;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chloroplast
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20-AUG-2001
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Pfam; PF01273; LBP_BPI_CETP;
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                                                                                  Pancic P.
                                                                                                               SEQUENCE OF 141-179 FROM N.A. MEDLINE=91192176; PubMed=1826
                                                                                                                                                                                     Plant Mol.
[3]
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., Strotmann H., Kowallik K.V.; subunit of the chloroplast ATPase Odontella sinensis."; 280:387-392(1991).
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(Rel. 25, Last sequence update)
(Rel. 40, Last annotation update)
B CHAIN (EC 3.6.1.34) (SUBUNIT I
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, TO THE BPI/CETP/LBP/PLTP FAMILY.
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f a chlorophyll
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Matches , 8; Conservative
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IR EMBL; Z67753; CAA91692.1; ...
IR EMBL; X57701; ...
IR EMBL; X57701; ...
IR PIR; S14444; S14444
S14444; S14444; S14444
S1388; S23358
IN Mendel; 4844; ODOS::atpF:1.
IN Mendel; A844; O
                                                                                                                                                                                                                                                    EMBL; X03241; CAA26998.1; -. PIR; A26027; VCBVCA.
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Best Local
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MEDLINE=86093657; PubMed=3841203;
Bergh S.T., Koziel M.G., Huang S.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
01-JAN-1988 (Rel. 05, Last sequence update)
COAT PROTEIN (CAPSID PROTEIN)
Viruses; ssrna positive-strand viruses, no DNA stage; Tobravirus.
                                                                                                                                                                                          Protein.
223 AA;
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les 8; Conserv
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SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE.
SIMILARITY: BELONGS TO THE ATPASE B CHAIN FAMILY.
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                                                                                                         42.78;
80.08;
                                                                                                                                                                                               23683 MW;
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61.58;
                                                                                     1;
                                                                                                       Score 41;
Pred. No.
                                                                                                                                                                             EF14652A2F743398 CRC64;
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Pred. No. 6
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                                                                                               DB 1; Length 223;
8.6;
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                                   VGLZ_IBVB

ID VGL2_IBVB

AC P11223; P05134; STANDARD; PRT; 1162 AA.

DT 01-JUL-1989 (Rel. 11, Created)

DT 01-JUL-1989 (Rel. 11, Last sequence update)

DE 20-AUG-2001 (Rel. 40, Last annotation update)

DE 22-AUG-2001 (Rel. 47, Last sequence update)

DE 22-AUG-2001 (Rel. 47, Last annotation update)

DE 23-AUG-2001 (Rel. 47, Last annotation update)

CONTROL OF THE PROTEIN PROTEIN)
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ID YD7

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DT 011

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SEQUENCE FROM N.A.
MEDLINE=87085499; PubMed=3025348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 6; Conserv
                                                            "Cloning and sequencing of the gene encoding the spike protein of the
                                                                                                                   Binns M.M., Boursnell M.E.G., Cavanagh D., Pappind D.J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=85159540; PubMed=2984314;
                                                                                                                                                                                                                                              Avian infectious bronchitis virus (strain Beaudette) (IBV).
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Skelton J., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V., Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
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Bukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
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01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last sequence update)
HYPOTHETICAL 82.5 KDA PROTEIN C32A11.01 IN CHROMOSOME
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720 AA; 82456 MW;
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P12651;
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-I- FUNCTION: THE PEPLOMER PROTEIN MEDIATES THE BINDING OF V
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modified and this statement is not removed. Usage by an
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SIGNAL
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EMBL; X02342;
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Pfam; PF01601; Corona_S2;
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InterPro; IPR002552; Corona_S2.
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(Rel. 12, Last sequence
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                                             STANDARD;
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PIKE PROTEIN SI
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MEDLINE-87021475; PubMed-2429473;

Niesters H.G.M., Lenstra J.A., Spaan W.J.M., Zijderveld A.J.,

Niesters H.G.M., Lenstra J.A., Spaan W.J.M., Zijderveld A.J.,

Bleumink-Pluym N.M.C., Hong F., van Scharrenburg G.J.M.,

Horzinek M.C., van der Zeijst B.A.M.;

"The peplomer protein sequence of the M41 strain of coronavirus

and its comparison with Beaudette strains.";

Virus Res. 5:253-263(1986).

-i- FUNCTION: THE PEPLOMER PROTEIN MEDIATES THE BINDING OF VIRIO
                                                                                                                                                                                                                                                                                                                    CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M21883; AAA66575.1; -.
EMBL; A24863; CAA01736.1; -.
PIR; S07421; S07421.
InterPro; IPR002551; Corona_S1.
InterPro; IPR002552; Corona_S2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-AUG-2001 (Rel. 40, Last annotation update)
E2 GLYCOPROTEIN PRECURSOR (SPIKE GLYCOPROTEIN) (PEPLOMER PROTEIN)
[CONTAINS: SPIKE PROTEIN S1; SPIKE PROTEIN S2].
                                                                                                                                                                                                                                                                                                                                                 Glycoprotein; Envelope
SIGNAL 1 18
                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF01600; Corona_S1;
Pfam; PF01601; Corona_S2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Viruses; ssRNA positive-strand Coronaviridae; Coronavirus.
                                                                                                                                                                                                      CARBOHYD
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Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
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YEAST

Query Match Best Local (

Matches

Similarity 6; Conser

42.78; 75.08;

Score 41; DB Pred. No. 50; 1; Mismatches

1;

Length 1162;

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Conservative

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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=S288C / FY1679;
MEDLINE=96109931; PubMed=8619317;
Bertani I. Coglievina M. Zaccaria P. Klima R. Bruschi C.V.;
"The sequence of an 11.1 kb fragment on the left arm of Saccharomyces of the chromosome VII reveals six open reading frames including frames including
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

MEDLING-91227124; PubMed-2027746;

Kipling D., Tambini C., Kearsey S.E.;

"rar mutations which increase artificial chromosome Saccharomyces cerevisiae identify transcription and proteins.";
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ROT-AUG-1991 (Rel. 19, Created)

O1-AUG-1991 (Rel. 19, Last sequence update)

STRAND EXCHANGE PROTEIN 1 (KAR(-) ENHANCING MUTATION PROTEIN)

EXORIBONUCLEASE) (DNA STRAND TRANSFER PROTEIN BETA) (STP-BETA)

KEMI OR SEPI OR XRM1 OR DST2 OR RAR5 OR YGL173C OR G1645.
                                                      from Saccharomyces cerevisiae.
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2, the gene for
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es cerevisiae.
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DNA strand
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                                   EXCHANGE AND 5'-3' EXONUCLEASE ACTIVITIES IN VITRO, PREFERENTIALLY EXCHANGE AND 5'-3' EXONUCLEASE ACTIVITIES IN VITRO, PREFERENTIALLY DEGRADES SINGLE-STRANDED DNA (SS-DNA) AND CAN RENATURE FROM CIRCULAR SS-DNA, CATALYSES THE FORMATION OF HETERODUPLEX DNA BEEN SHOWN TO BE A G4-DNA-DEPENDENT NUCLEASE AND A 5'-3' CHROMOSOME STABILITY AND DEFECTS IN SPINDLE POLE BODY DUPLICATION EXORREDION. MUTARION AFFECT NUCLEAR FUSION, LEED TO REDUCED AND/OR SEPARATION AS WELL AS LOSS OF VIABILITY UNDER COMDITIONS OF WITH CYTOPLASMIC MICROTUBULE-ASSOCIATED PROTEIN WHICH INTERACTS OF WITH CYTOPLASMIC MICROTUBULE-ASSOCIATED PROTEIN WHICH INTERACTS MAGNESIUM (MG(2+)), FOR THE STRAND EXCHANGE ACTIVITIES REQUIRE REPLACE MG2+ WHEN THE LINEAR DS-DNA HAS BEEN FIRST RESECTED WITH
                                                                                                                                                                                                                                                                                                                                                                                                                               Heyer W.-D.;
                                                                                                                                                                                                                                                                                                                                                                                      Saccharomyces
EMBO J. 14:10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ASSOCIATION WITH MICROTUBULES. MEDLINE=95237186; PubMed=7720696;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cerevisiae strand exchange protein 1 (Sep1/xrn1/Kem1), multifunctional exonuclease."; Mol. Cell. Biol. 15:2728-2736(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interthal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=95257954; PubMed=7739553; Heyer W.-D., Johnson A.W., Reinha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              eyer W.-D., Johnson A.W., Reinhart U., Kolodner R.D., Regulation and intracellular localization of Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHARACTERIZATION OF SPECIFICITY F
MEDLINE=94291198; PubMed=8020096;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHARACTERIZATION OF EXONUCLEASE AND MEDLINE-94245729; PubMed-8188690; Kaeslin E., Heyer W.-D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Liu Z., Gilbert W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pombe cells exhibiting in vitro strand. J. Biol. Chem. 269:14094-14102(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             strand exchange protein 1 with DNA.
J. Biol. Chem. 269:3673-3681(1994).
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JOhnson A.W., Kolodner R.D.,
"Characterization of the interaction of th
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MEDLINE-93013019; PubMed-1398123;
Larimer F.W. Hsu C.L., Maupin M.K., Stevens A.,
"Characterization of the XRNI gene encoding a 5'-->3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Johnson
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14:1057-1066(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          son A.W., Kolodner R.D., activity of the Saccharomyces
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120:51-57(1992)
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ces cerevisiae.";
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gene-disrupted yeast cells.";
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PREDOMINANTLY CYTOPLASMIC,
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MEDLINE=91203879; PubMed=1850100; Dykstra C.C., Kitada K., Clark A.B.,

KSTra C.C., Kitada K., Clark A.B., Haman Joning and characterization of DST2, the ansfer protein beta from Saccharomyces L. Cell. Biol. 11:2583-2592(1991).

SEQUENCE FROM N.A.

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protein

"Kim J., Ljungdahl P.O., Fink G.R.,
"kem mutations affect nuclear fusion in
Genetics 126:799-812(1990).

PubMed=2076815; P.O., Fink G.R.;

MEDLINE=91169260; SEQUENCE FROM N.A.

Saccharomycetales;

Saccharomycetaceae;

Saccharomycotina;

Eukaryota; Fungi; Ascomycota;

"Disruption of the gene XRN1, "Disruption of the gene XRN1, restricts yeast cell growth.";

coding

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5'-->3'

ricts yeast celí 95:85-90(1990).

MEDLINE=91071610;

PubMed=1979303;

SEQUENCE FROM N.A.

CHARACTERIZATION OF MEDLINE=91310695;
Johnson A.W., Kolo

Kolodner R.D.

ALSO PERINUCLEAR

Nucleic Acids Res.

SIMILARITY: STRONG S.POMBE DHP1.

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EMBL; X54717; CAA38520.1; -.
EMBL; M58367; AAA35036.1; -.
EMBL; M36725; AAA35125.1; -.
EMBL; X61181; CAA43487.1; -.
EMBL; X61181; CAA43487.1; -.
EMBL; X61181; CAA59180.1; -.
EMBL; X72695; CAA59885.1; -.
EMBL; Z72695; CAA96885.1; -.
EMBL; Z73695; CAA96885.1; -.
EMBL; Z73695; SAA9685.1; -.
PIR; S13743; S13743.
PIR; S16701; S16701.
PIR; S16701; S16701.
PIR; A39790; A39790.
SGD; S0003141; KEM1.
Virology
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P19523; Q83208; P89877; P90356;
01-FEB-1991 (Rel. 17, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
RNA-DIRECTED RNA POLYMERASE (EC 2.77.48) (186 KDA PROTEIN) (CONTAINS:
METHYLTRANSFERASE/RNA HELICASE (MT/HEL) (129 KDA PROTEIN)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGMVS
                       MEDLINE-89073773; PubMed=3201760; Saito T., Imai Y., Meshi T., Okada Y.; Imai P., Meshi T., Okada Y.; Virology 167:653-656(1988).
                                                                                                                                                                                                 Ugaki M., Tomiyama M., Kaku
Sato T., Motoyoshi F., Nish
Submitted (FEB-1997) to the
                                                                                                                                                                                                                                                                          STRAIN-SH;
                                                                                                                                                                                                                                                                                                                                                                           "The complete nucleotide sequence of cucumber green mottle mosaic virus (SH strain) genomic RNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sato
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cucumber green mottle mosaic virus (watermelon strain Cucumber green mottle mosaic virus (watermelon strain Viruses; ssRNA positive-strand viruses, no DNA stage; NCBI_TaxID=12236, 12237;
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SEQUENCE 1528 AA; 175459 MW;
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T., Motoyoshi F.,
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9; Conservative
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                                                                                                                                                     OF 1496-1648 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                      72:1487-1495(1991).
                                                                                                                                                                                                    M., Kakutani T., Hidaka S.,
F., Nishiguchi M.;
7) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Nishiguchi
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PROTEIN IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 41; DB Pred. No. 67; 1; Mismatches
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RNA
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67;
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                                                 of tobamoviruses.";
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                                                                                                                                                                                                                                                Kiguchi T.,
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EMBL; D12505; BAA18896.1; -.
EMBL; D12505; BAA18896.1; -.
EMBL; J04322; AAA46382.1; -.
PIR; JQ1157; WMTMS2.
InterPro; IPR001788; RNA_dep_RNApo12.
InterPro; IPR002588; V_methyltransf.
InterPro; IPR000566; Viral_helcse1.
InterPro; IPR000666; Viral_helcse1.
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P46939;
01-NOV-1995 (Rel. 3
01-NOV-1995 (Rel. 3
20-AUG-2001 (Rel. 4
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CHAIN
NP_BIND
SEQUENCE
                 "The 2.0-A structure of the second calponin homology domain fro actin binding region of the dystrophin homologue utrophin.";
J. Mol. Biol. 285:1257-1264(1999).
-i- FUNCTION: MAY PLAY A ROLE IN ANCHORING THE CYTOSKELETON TO PLASMA MEMBRANE (BY SIMILARITY TO DYSTROPHIN).
-i- SUBCELLULAR LOCATION: NEUROMUSCULAR JUNCTION.
                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 144-261.
MEDLINE=99141377; PubMed=9887274;
Keep N.H., Norwood F.L.M., Moores C.A., Winder S.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation updat
UTROPHIN (DYSTROPHIN-RELATED PROTEIN 1) (DF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1188
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Pfam: PF011443; Viral_helicase1; 1.
Pfam: PF01660; Vmethyltransf; 1.
Transferase; RNA-directed RNA polymerase; Helicase; ATP-binding.
CHAIN 1 1648 RNA-DIRECTED RNA POLYMERASE.
CHAIN 1 1648 RNA-DIRECTED RNA POLYMERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                     Tinsley J.M., Blake D.J., Roche A., Fai
Byth B.C., Knight A.E., Kendrick-Jones
Edwards Y.H., Davies K.E.,
"Primary structure of dystrophin-relate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UTRN OR DMDL.
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                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE=93096045; PubMed=1461283;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
                                                                                                                                                             Kendrick-Jones J.;
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FUNCTION: THE SMALLER PROTEIN IS A METHYLTRAN CAPPING AND AN RNA HELICASE.

MISCELLANEOUS: READTHROUGH OF THE TERMINATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CODONS
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                                                                                                                                                                                                                                                                                    360:591-593(1992).
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8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 equires a license agreement (See http://www.isb-sib.ch/announce/email to license@isb-sib.ch).
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SPECIFICITY:
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Primates;
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70 ATP (POTENTIAL).

186549 MW; 1D1AFFEEE7B65595 CRC64;
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  MUSCLE
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Catarrhini;
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Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                 Fairbrother U.,
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i; Hominidae; Homo.
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Query Match
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SMART; SM00033; CH; 2.
SMART; SM00150; SPEC; 18.
SMART; SM00150; SPEC; 18.
SMART; SM00291; ZnF_Zz; 1.
SMART; SM00291; ZnF_Zz; 1.
SMART; SM00291; ZnF_Zz; 1.
PROSITE; PS00019; ACTININ_1; 1.
PROSITE; PS00020; ACTININ_2; 1.
PROSITE; PS00020; CH; 2.
PROSITE; PS01159; WM_DOMAIN_1; 1.
SROSITE; PS01159; WM_DOMAIN_2; 1.
SROSITE; PS01159; WM_DOMAIN_2; 1.
SROSITE; PS01159; WM_DOMAIN_2; 1.
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InterPro; IPR001715; C
InterPro; IPR002017; S
InterPro; IPR003122; T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00307; CH; 2. Pfam; PF00435; spectrin; 19. Pfam; PF00397; WW; 1 19. Pfam; PF00369; ZZ; 1. Pfam; PF00569; ZZ; 1.
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InterPro;
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InterPro; IPR000433;
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SIMILARITY: THE ACTIN-BINDING DOMAIN IS OF A TYPE FOUND IN MANY ACTIN-BINDING PROTEINS (SUCH AS ACTININ, DYSTROPHIN, FIMBRIN, ABP-120, ABP-180, OR BETA-FOORIN).
SIMILARITY: CONTAINS 1 WW DOMAIN.
SIMILARITY: CONTAINS 20 SPECTRIN REPEATS.
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                                            Conservative
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WW_domain.
ZnF_ZZ.
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Calponin_hom.
Spectrin.
TarH.
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Pred. No. 1.6e+02;
3; Mismatches 5;
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AC 09ZDIO)
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CC Bacter
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01-NOV-1995 (Rel. 32, Last annotation upc
MAJOR FIMBRIAL SUBUNIT PRECURSOR (PILIN)
HIFA.
Haemophilus influenzae
                                                                                            HFA3_HAEIN
P45988;
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                                                                                               STANDARD;
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RY STRAIN-MADELD E;

RY MEDLINE-99039499; PubMed-9823893;

RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,

RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,

RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,

RA Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,

RT The genome sequence of Rickettsia prowazekii and the origin of

"The genome sequence of Rickettsia prowazekii and the origin of

RT Thickettsia Prowazekii and the origin of

RT THE 396:133-140(1998).

CC PART OF THE 30S SUBUNIT PRIOR TO RURING THE FINAL STEP IN THE

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CC SUBUNIT SUT NOT FOR 70S RIBOSOMES (BY SIMILARITY).

CC -: SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).

CC -: SIMILARITY: BELONGS TO THE RIMM FAMILY.
                                                                                                                                                                 the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PROBABLE 16S RRNA PROCESSING PROTEIN RIMM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rickettsia prowazekii.
Bacteria; Proteobacteria; alpha subdivision; Rickettsiaceae; Rickettsieae; Rickettsia.
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20-AUG-2001
20-AUG-2001
20-AUG-2001
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Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: MEDIATES ADHERENCE TO OROPHARYNGEAL EPITHELIAL CELLS
-HELPS THE AIRWAY COLONIZATION PROCESS.
-I- SUBCELLULAR LOCATION: FIMBRIA.
                                          the European Bioinformatics Institute. There are no rest use by non-profit institutions as load as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isborsend an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                           Sulfolobus acidocaldarius
Archaea; Crenarchaeota; Su
                                                                                                                                                                                                                                                                                   FIBRILLARIN-LIKE FLPA OR FIB.
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InterPro; IPRO
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nes 8; Conserv
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                                                                                                                                                                          of small nucleolar RNAs in Archaea.";
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42
212 AA;
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(Rel. 40, Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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212
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           Fibrillarin
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Pred. No.
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MAJOR FIMBRIAL SUBUNIT.
PROBABLE.
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PROTEIN.
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KMS1_SCHPO STANDARD; PRT; 6
P87245;
20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence up
20-AUG-2001 (Rel. 40, Last annotation
KARYOGAMY MEIOTIC SEGREGATION PROTEIN
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                                                                                                                                                                                                                 EMBL; D84439; BAA20460.1;
EMBL; Z99260; CAB16381.1;
Cell division; Meiosis.
SEQUENCE 607 AA; 69240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oliver K., Harris D., Barrell B.G., Rajandream M.A., Wood V.;
Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
1: FUNCTION: HAS A ROLE IN KARYGGAMY, RECOMBINATION AND SEGRATION
DURING MEIOSIS, ALTHOUGH IT HAS BEEN SHOWN TO ASSOCIATE WITH THE
SPINDLE POLE BODY IT IS UNLIKELY TO BE INVOLVED IN ITS FORMATION
OR MAINTENANCE SINCE KMS1(-) MUTANTS ARE ABLE TO COMPLETE MITOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "A novel fission yeast gene, kms1+, is required f meiotic prophase-specific nuclear architecture."; Mol. Gen. Genet. 254:238-249(1997).
                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Horio T., Niwa O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND FUNCTION. MEDLINE=97294501; PubMed=9150257;
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Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
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70
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                                                                                            1;
                                                                                               Pred. No. 37;
l; Mismatches
                                                                                                                      Score 40;
Pred. No.
                                                                                                                                                                                                                        216A1D5CA93C9550
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HS83_DROAV
ID HS83_DROAV
AC 002192;
DT 15-DEC:
DT 15-DE

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"SV2, a brain synar
                                                                                                                                                     Q02563;
Q1-EBH-1995 (Rel. 31, C
Q1-EBH-1995 (Rel. 31, L
30-MAY-2000 (Rel. 39, L
                                                              SEQUENCE FROM N.A., AND SEQUENCE
                                                                                               Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata,
Mammalia; Eutheria; Rodentia;
                                                                                            NCBI_TaxID=10116;
                                                                                                                                    01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
SYNAPTIC VESICLE PROTEIN 2 (SV2).
                                                                                                                                                                                                                                                                                                                                     PRINTS; PRO0775; HEATSHOCK90.
SMART; SM00387; HATPASS_C; 1.
PROSITE; PS00298; HSP90; 1.
Chaperone; ATP-binding; Heat shock.
SEQUENCE 716 AA; 81760 MW; 9EC59F027C4DFCD7 CRC64;
                                                                                                                                                                                                                                                     457 DFCSLSDYVSRMKENQ 472
                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPRO03594; HATPase_c. Pfam; PF02518; HATPase_c. Pfam; PF02518; HATPase_c; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation are by non-profit institutions as long as its content is in no was or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 FlyBase; FBgn0020208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U75687; AAB58358.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The hsp83 gene of Drosophila auraria.",
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
-- FUNCTION: MOLECULAR CHAPERONE. HAS ATPASE ACTIVITY
-- SUBCELLULAR LOCATION: CYTOPLASMIC.
-- SUBCELLULAR LOCATION: CYTOPLASMIC.
-- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 90 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      002192;
15-DEC-1998 (Rel. 37, C.
15-DEC-1998 (Rel. 37, L.
15-DEC-1998 (Rel. 37, L.
HEAT SHOCK PROTEIN 83 (
                                                                                                                                                                                                                                                                          2 EHCNFNDVTTRLRENE 17
               lieh S.M., Peterson K., Shingal R., Scheller a brain synaptic vesicle protein homologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila auraria (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN=3040.11B;
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5; Conserv
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                                           PubMed=1519064;
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31.28;
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Last annotation update)
(HSP 82).
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                                                                                  Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rat
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                                                                                                                                                                                                                                                                                                     Score 40;
Pred. No.
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  RESULT 22
Y594_METJA
ID Y594_METJA
AC 058012;
DT 01-NOV-1997 (1)
DT 02-NOV-1997 (1)
DT 20-AUG-2001 (1)
DT 20-AUG-2001 (1)
DE HYFOTHETICAL F
GN MJ0594
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Best Local
           Methanococcus jannaschii.
Archaea; Euryarchaeota; N
       Methanococcus
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions. There are no restrictions on its entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transporters.";
Science 257:1271-1273(1992).
-I-FUNCTION: MAY ACT AS A VESICLE-LOCALIZED NEUROTRANSMITTER
TRANSPORTER OR MAY FUNCTION AS AN ION TRANSPORTER OR CHANNEL
-I-SUBCELLULAR LOCATION: SYNAPTIC VESICLE.
SPINAL CORD.
                                                                                                                                                                                                   Similarity
7; Conserv
                                        (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 40, Last annotation updat.
L PROTEIN MJ0594.
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63.68;
Methanococcales; Methanococcaceae;
                                                                                                                                                                                                                                                   MW;
                                                                                                                                                                                      Score 40; DB Pred. No. 46; 1; Mismatches
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N-LINKED (GLCNAC...) (PO
N-LINKED (GLCNAC...) (PO
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Query Match
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[1]
SEQUENCE FROM
STRAIN=JAL-1
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30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 40, Last annotation update)
20-AUG-2001 (Rel. 40, Last annotation update)
PROBABLE GUANOSINE-3', 5'-BIS(DIPHOSPHATE) 3'-PYROPHOSPHOHYDROLASE
(EC 3.1.7.2) ((PPGPP)ASE) (PENTA-PHOSPHATE GUANOSINE-3'-PYROPHOSPOHYDROLASE).
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MEDLINE-96337999; PubMed-8688087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                    Synechocystis sp. strain PCC6803. II. Sequence entire genome and assignment of potential prote DNA Res. 3:109-136(1996).
                                                                                                                                                                                                                                                                                                                                                          Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nal
Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura
Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K
Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M.,
Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      _SYNY3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rram; PF01045; IMP4; 1.
Hypothetical protein; Complete
SEQUENCE 169 AA; 20053 km²
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPOT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synechocystis sp. (strain Bacteria; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U67508;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science 273:1058-1073(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=97061201; PubMed=8905231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=1148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119
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                                                                                                             RES. 3:109-136(1996).

FUNCTION: IN EUBACTERIA PPGPP (GUANOSINE 3'-DIPHOSPHATE 5-DIPHOSPHATE) IS A MEDIATOR OF THE STRINGENT RESPONSE THAT COORDINATES A VARIETY OF CELLULAR ACTIVITIES IN RESPONSE 1
                                         DEGRADATION OF
                                                                               CHANGES
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                                                                           IN NUTRITIONAL ABUNDANCE.
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                                         PPGPP INTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41.18;
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Chroococcales;
       O GDP.
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Pred. No. 1
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9FF6090865C6E4B0 CRC64;
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                                         T
   THIS ENZYME CATALYSES
MAY ALSO BE CAPABLE OF
(BY SIMILARITY).
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                                                                                                             STRINGENT RESPONSE THAT ACTIVITIES IN RESPONSE TO
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There are no restrictions
ng as its content is in
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Best Local
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V_SIVCZ
V_SIVCZ
STANDARD; PRT; 854 AA.
P17281;
01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
ENVELOPE POLYPROTEIN GP160 PRECURSOR [CONTAINS: EXTERIOR MEMBRANE ENVELOPE POLYPROTEIN GP1201; TRANSMEMBRANE GLYCOPROTEIN (GP41)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                               Signal.
SIGNAL
CHAIN
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Hydrolase; Manganese; Complete
SEQUENCE 760 AA; 86568 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; D90911; BAA18078.1; InterPro; IPR002912; ACT. InterPro; IPR003607; HDc. Pfam; PF01842; ACT; 1.
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                                                                                                                                                                                                                           EMBL; X52154; CAA36407.1;
PIR; S09990; VCLJSI.
HIV; X52154; ENV$CPZ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genetic organization of a Nature 345:356-359(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=90259077; PubMed=2188136; Huet T., Cheynier R., Meyerhans A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV). Viruses; Retroid viruses; Retroviridae; Lentivirus.
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                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                entities
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European Bioinformatics Institute. There are no restrict
by non-profit institutions as long as its content is
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COFACTOR: MANGANESE (BY SIMILARITY).
SIMILARITY: BELONGS TO THE RELA / SPOT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       European Bioinformatics Institute. There are no restrictions
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                                                                                                                                     PF00516; GP120; PF00517; GP41; 3
                                                                                                                  Coat
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                                                                                                                                                                                   IPR000328; Env_GP IPR000777; GP120.
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500
854
517
                                                                                                                Polyprotein;
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31.2%;
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Pred. No. 57;
1; Mismatches
    TRANSMEMBRANE POTENTIAL.
                                               EXTERIOR MEMBRANE
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CA276EA2286358F7
                                                                                                                  Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Roelants G., Wain-Hobson S.; ee lentivirus related to HIV-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.5;
57;
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                          GLYCOPROTEIN
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Best Local S
Matches 8
chromosomal mapping, complement-in activity.", complement-in Transplantation 66:1094-1100(1998)
                                                                           TISUE-Aortic endothelium;
MEDLINE-98217182; PubMed-9558099;
Hinchliffe S.J., Rushmere N.K., Hanna S.M., Morgan Molecular cloning and functional characterization analogue of CD59: relevance to xenotransplantation.
J. Immunol. 160:3924-3932(1998).
                       "Structure/function characterization
                                      MEDLINE=9023683; PubMed=9808497; Maher S.E., Pflugh D.L., Larsen N Bothwell A.L.M.;
                                                              SEQUENCE OF 26-123 FROM N.A., AND FUNCTION
                                                                                                                                                                                    CD59_PIG STANDARD; PRT; 123 AA.
062680; 09XT94; 09TR76;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
CD59 GLYCOPROTEIN PRECURSOR (MEMBRANE ATTACK COMPLEX INHIBITION PROTEIN) (MAC-IP) (PROTECTIN).
                                                                                                                                                       NCBI_TaxID=9823;
                                                                                                                                                               Sus scrofa (Pig).
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
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Cetartiodactyla; Suina; Suidae; Sus.
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RA van den Berg C.W., Harrison R.A., Morgan B.P.;
RT preparative SDS-PAGE: application of analogues of human CD59 by
RT J. Immunol. Methods 179:223-231(1995)
CC -1- FUNCTION: POTENT INHIBITOR OF THE COMPLEMENT MEMBRANE ATTACK
CC COMPLEX (MAC) ACTION. ACTS BY BINDING TO THE C8 AND/OR C9
CC COMPLEX (MAC) ACTION. ACTS BY BINDING TO THE C8 AND/OR C9
CC COMPLEX (MAC) ACTION OF THE MOLTIPLE COPIES OF C9 REQUIRED FOR COMPLETE
CC INCORPORATION OF THE MULTIPLE COPIES OF C9 REQUIRED FOR COMPLETE
CC FORMATION OF THE OSMOLYTIC PORE.
CC ITISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES TESTED (LUNG, TESTIS
CC LIVER, KIDNEY, SPLEEN, HEART AND SKELETAL MUSCLE). HIGHEST LEVELS
CC -1- SIMILARITY: CONTAINS 1 UPAR/LY6 DOMAIN.
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InterPro; IPRO01526; LY6_UPAK.
Pfam; PF00021; UPAR_LY6; 1.
SMART; SM00134; LU; 1.
PROSITE; PS00983; LY6_UPAR; 1.
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EMBL; AF058328; AAD39837.1; -...
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H -> Y (IN REF. 3)
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MISSING (IN REF. 3)
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REMOVED IN MATURE FORM (BY SIMILARITY).
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FD62ED3F93C91321 CRC64;
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Post-processing: Minimum Match 0%
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Listing first 50 summaries
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6: sp_mammal:*
7: sp_mhc:*
8: sp_organel14
9: sp_plant:*
10: sp_plant:*
11: sp_rodent:
12: sp_vertebr:
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14: sp_unclass:
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.

46.5 48.4 45.8 46.5 47.5 444.3 3.4 44.3	Query Score Match
721 1762 284 777 1305 205 513 530 807 1101 1101 545 545 547 548 739 96 240 240	% Query Match Length DB
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027308 anopheles a Q19346 caenorhabdi O915m0 pseudomonas O9ker0 bacillus ha Q93554 caenorhabdi O9zcg3 rickettsia Q82618 avian infec O5343 avian infec O5343 avian infec O9791 methanobact Q9ndq3 ciona intes O82667 avian infec Q82667 avian infec Q92669 avian infec Q9y9e6 drosophila O70950 human immun P90082 human immun P90085 human immun P90085 human immun P90085 human immun P90085 human immun P90088 human immun	Description

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human	Q9iual human immun		human	N	016166 drosophila		-	Q9tk23 diphysa flo			Q9tk27 ormocarpum	Q9tk28 ormocarpum	Q9tk29 ormocarpum		Q9tk31 ormocarpops	Q9kg62 bacillus ha	Q9tk00 ormocarpum			Q9tjz8 pictetia ac		Q9gi57 humularia c	Q9ykv1 human immun	Q9ik03 human immun	Q9ik04 human immun	Q9ik05 human immun	Q73350 human immun	Q9ik06 human immun	Q9ik02 human immun	Q9s091 borrelia bu

ALIGNMENTS

SQ SEQUENCE	DR SMART			DR Pfam;			HSSP;	EMBL;			RT genes.";	RT "Precise		RX MEDLI		70	OX NCBI_			OC Eukary	OS Anopheles	GN HSP82		DT 01-JU			ID Q27308	RESULT 1 Q27308
HEAT STOCK. SEQUENCE 721 AA; 82153 MW; C71867C5610452EA CRC64;	 SMART; SMUU387; HATPase_C; I.	PRINTS; PRO0775; HEATSHOCK90.	Pfam; PF00183; HSP90; 1.	Pfam; PF02518; HATPase_c; 1.	InterPro; IPR001404; HSP90.	InterPro; IPR003594; HATPase_c.	; P07900; 1YER.	L47285;	L47285	ct Mol. Biol. 5:73-79(1996).		cise limitation of concerted evolution to ORFs in mosquito Hsp82	Benedict M.Q., Levine B.J., Ke Z.X., Cockburn A.F., Seawright J.A.;	MEDLINE=96209490; PubMed=8630537;	STRAIN=SANTA TECLA;	ENCE FROM N.A.	NCBI_TaxID=7167;	•	Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;	; Metazoa;	heles albimanus (New world malaria mosquito).	2.	PROTEIN 82.	(TrEMBLrel. 17, Last	OV-1996 (TrEMBLrel. 01, Created)	08;	08 PRELIMINARY; PRT; 721 AA.	1

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Best Loc Matches

Local

43.8%;

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Query Match
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Matches 12; Conserv:
                                               MEDLINE-20437337; PubMed=10984043;

Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.

Brody L.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.

Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.,

Complete genome sequence of Pseudomonas aeruginosa PAO1, an

Opportunistic pathogen.",

Nature 406:959-964(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9ISMO;

01-MAR-2001 (TrEMBLTel. 16
01-MAR-2001 (TrEMBLTel. 16
01-JUN-2001 (TrEMBLTel. 17
PROBABLE TRANSCRIPTIONAL R
PA0708.
                                                                                                                                                                                                                                                                                                            STRAIN-PAO1;
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Bacteria; Proteobacteria;
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VARSPLIC
SEQUENCE
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EMBL; Z54270; CAA91030.1; -.
EMBL; Z54270; CAA91031.1; -.
InterPro; IPR00517; Ribosomal_L30.
PROSITE; PR002035; VWFA.
PROSITE; PS00634; RIBOSOMAL_L30; UNKNOWN_1.
SMART; SM00377; VWFA; 1.
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VARSPLIC 1301 1302
VARSPLIC 1303 1767
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Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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01-JUN-2001
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Q19346;
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Q1-FEB-1997 (TrEMBLrel. 0
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F23A7.5 PROTEIN.
E23A7.5.
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Submitted
                                                                     SEQUENCE FROM N.A.
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Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
Eukaryota; Mejoderinae; Caenorhabditis.
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STRAIN=C-125 / JCM 9153;
MEDLINE=20512582; PubMed=11058132;
Takami H., Nakasone K., Takaki Y., Maeno G.
Fuji F., Hirama C., Nakamura Y., Ogasawara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   halodurans and genomic sequence comparison Nucleic Acids Res. 28:4317-4331(2000).
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Bactllus halodurans.
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
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01-OCT-2000
01-OCT-2000
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5; Mismatches
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01-NOV-1996
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01-MAY-1999
01-MAY-1999
01-JUN-2001
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Bonfield J., Button J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Ropara A., Saunders D., Shownkeen R.,
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
                                                                                                                                                                          Nature 396:133-140(1998).
EMBL; AJ235273; CAA15216.1; -
InterPro; IPR001457; Oxidored_q3.
Pfam; PF00499; oxidored_q3; 1.
                                                                                                                                                                                                                                    Andersson S.G.E., Zomorodipour A., Andersson J.O., Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Eriksson A.-S., Winkler H.H., Kurland C.G.;
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STRAIN-MADRID
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EMBL; Z81067; CAB02976.1; -
SEQUENCE 1307 AA; 147397
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"Evolutionary implications of genetic variations i infectious bronchitis virus.", virus Res. 34:327-338(1994).
EMBL; L1899; AAN4378.1; -.
InterPro; IPR002551; Corona_S1.
Pfam; PF01600; Corona_S1; 1.
SEQUENCE 513 AA; 56541 MW; 2D4C1F002777
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01-JUN-1998 (TremBLrel. 06, Last sequence update)
01-JUN-2001 (TremBLrel. 17, Last annotation update)
SPIKE GLYCOPROTEIN S1 SUBUNIT (FRAGMENT).
avian infectious bronchitis virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae; Coronavirus.
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Viruses; ssRNA positive-strand viruses,
Coronaviridae; Coronavirus.
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MOORE K.M., Jackwood M.W., Bennett J.D., Seal Submitted (OCT-1997) to the EMBL/GenBank/DDBJ EMBL; AF027512; AAB87907.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=11120;
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                   Similarity
6; Conserv
(TrEMBLrel.) (TrEMBLrel.)
                                                                                                                                                                                                                                                           530 AA;
                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                             103
                                                                                                                                                                                                                                                           58315 MW;
                                                                                                                                                                                                   45
75
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75
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 05,
05,
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Last sequence update)
Last annotation updat
                            Created)
                                                                                                                                                                                   2;
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Pred.
                                                         PRT;
                                                                                                                                                                                                                                                           74CE496CE25688F5 CRC64;
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31;
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  update)
                                                                                                                                                                                                                                                                                                                                 B.S.;
databases.
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                                                                                                                                                                                                               Length 530
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                                                                                                                                                                                      Indels
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thermoautotrophicum

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PRESULT 10
09NDQ3
AC Q9NDQ3
DT 01-OCT
DT 01-OC
                                                                                                                                                        RT "Characterization of Brachyury downstream notochord genes in the Ciona intestinalis embryo.";

RT intestinalis embryo.";

RT Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.

CC -: SIMILARITY: TO OTHER SUBUNITS (ALPHA) OF SUCCINYL-COA SYNTHETASE,

CC -: SIMILARITY: TO OTHER SUBUNITS (BETA) OF SUCCINYL-COA SYNTHETASE,

CC OF MALATE--COA LIGASE AND TO ATP CITRATE-LYASE.

DR EMBL; AB036847; BAB00624.1; -.

DR InterPro; IPR00303; COA_1igase.

DR InterPro; IPR00303; COA_1igase.

DR Ffam; PR001901; CPSASE.

DR PROSITE; PS00267; CPSASE_2; UNKNOWN_1.

DR PROSITE; PS01216; SUCCINYL_COA_LIG_1; UNKNOWN_1.

KW Ligase: Lyase: Phosphorulation_LIG_3; 1.
           Query Match
Best Local Similarity
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Best Local Similarity
Workches 8; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RA Smith D.R., Doucette-Stamm L.A., DeLoughery C., Lee H.-M., DuBois J., RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., RA Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D., RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Glybon R., Vicare R., Wang Y., Wierzbowski J., Glybon R., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., Church G.M., Safer H., Patwell D., Prabhakar S., Church G.M., RA Daniels C.J., Mao J.-I., Rice P., Nolling J., Reeve J.N., RT "Complete genome sequence of Methanobacterium thermoautotrophicum deltaH: functional analysis and comparative genomics."; D. Bacteriol. 179:7135-7155(1997).

DR BABEL; AE000931; AAB6629.1; DR MABER29.1; DR Pfam; PF01136; Peptidase_U32: 1.

DR PROSTTE; PS01276; PEPTIDASE_U32: UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9NDQ3 PRELIMINARY;
Q9NDQ3;
01-CCT-2000 (TrEMBLrel. 15, C
01-CCT-2000 (TrEMBLrel. 15, L
01-JUN-2001 (TrEMBLrel. 17, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
HOTTA K., Takahashi H., Asakura T., Saitoh B., Takatori N., Satou Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ciona intestinalis.
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Phlebobranchia;
MCBI_TaxID=7719;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATP CITRATE-LYASE.
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MEDLINE-98037514; PubMed-9371463;

Smith D.R., Doucette-Stamm L.A., DeLoughery C., Lee H.-M., Duffert K., Gilbert K., Gilbert K., Silbert K., Sil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 FEHCNFNDVTTRLRE 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae; Methanothermobacter.
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                                                                                                                                                 Phosphorylation.
1 AA; 120728 MW;
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               45.8%;
50.0%;
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53.3%;
Score 44;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
Last sequence update)
Last annotation updat
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Pred. No. 47;
                                                                                                                     63CFF1B8D285DF49 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1101 AA.
DB 5;
64;
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               Length 1101;
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AD 82667

ID 2667

ID 2667

AC 088

AC 089

AC
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Q82619
ID Q82619
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Query Match
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Best Local s
Matches 6
                                          STRAIN-HOLTE;
STRAIN-HOLTE;
Wang L., Collisson E.W.;
Submitted (JUN-1993) to the EMBL/GenBank/DDBJ databases.
EMBL; L1898; AAA74379.1;
InterPro; IPR002551; Corona_S1.
                                                                                                                                                                                                                          Q82619 PRELIMINARY; PRT; 545 AA.
01-NOV-1996 (TrEMBLrel. 01, Created)
01-VOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2011 (TrEMBLRel. 17, Last annotation update)
                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                  avian infectious bronchitis virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                              101 HCNFTDIT 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-93298060; PubMed-8390829; (Cavanagh D., Davis p.J.; "Sequence analysis of strains of avian infectious bronchitis coronavirus isolated during the 1960s in the U.K."; EMBL; X64737; CAA46003.1; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Signal; Membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF01600; Corona_S1; 1.
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01-NOV-1996 (TYEMBLYEL 0
01-JUN-2001 (TYEMBLYEL 1
SPIKE PROTEIN SUBUNIT 1 P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            avian infectious bronchitis virus.
Viruses; ssRNA positive-strand viruses,
Coronaviridae; Coronavirus.
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01-NOV-1996
01-NOV-1996
01-JUN-2001
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STRAIN=UK/918/67;
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                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 75.06; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CSFNELNTKIRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          544 AA;
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>544 SPIKE PROTEIN SUBUNIT 1.
544 OAOAZEZ6344CEOOB CRC64;
        44.88;
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75.08;
  Score 43;
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01,
17,
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Pred. No. 46;
1; Mismatches
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                                C40BFB969ABA9647 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
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DB 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              no DNA stage; Nidovirales;
                                                                                                                                                                                                                                                                                                                                                                                                                          12;
                                                                                                                                                                                                                                                                                                                                                                                                                     Length 544;
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RESULT
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                                                                                                                                                       RA Goldek A., Gong F., Garg N.S., Gelbart W.M., Glasser M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibeqwam C.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibeqwam C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeqwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA McIntosh T.C., McLeod M.P., McPherson D.,
RA McHxulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA McHxulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Sylrskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Yiriskas R., Johng F.N., Zhong W., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Rubin G.M., Venter J.C.;
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
REMBL; AE003787; AAF57345.1;
DR FilyBase; FBgn0033010; CG3136.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies S.,
de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.
Durbin K.J., Evangelista C.C., Ferza C., Ferriera S., Fleischmann W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          George R.A., Lewis S.E., Richard J.C., Danag Q., Chen L.X., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Brandon R.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Wan K.H., Miklos G.L.G., Wan K.H., Miklos G.L.G., Wan K.H., W
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CG3136 PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ephydroidea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101 HCNFTDIT 108
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                                                                                  Pro; IPR001871; bZIP. PF00170; bZIP; 1.
                                             SM00338;
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                                             BRLZ;
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17,
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    63D67E2EE08F84F7 CRC64;
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Query Match

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P90081;
T 01-MAY-1997 (TrEMBLrel. U., Last beg O1-MAY-1997 (TrEMBLrel. 13, Last ann O1-JUN-2001 (TrEMBLrel. 17, Last ann PAVELOPE GLYCOPROTEIN (FRAGMENT).
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InterPro; Iraco
ofam; PF00516;
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Q70950;
01-NOV-1996
01-NOV-1996
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                                                                                                                                                                                    McDonald R.A., Mayers D.L., Chung R.C.Y., Wagner K.F., kim S., Birx D.L., Michael N.L.; michael N.L.; Evolution of human immunodeficiency virus type 1 env sequence variation in patients with diverse rates of disease progression
                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-PATIENT A;
MEDLINE-97184515; PubMed-9032317;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae;
NCBI_TaxID=11676;
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Viruses; Retroid viruses; Retroviridae; Lentivirus
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01-NOV-1996 (TrEMBLrel. 11, Last sequence up)
01-UN-2001 (TrEMBLrel. 17, Last annotation of the control 
                                                                                      J. Virol. 71:1871-1879(1996).
EMBL; U69285; AAC56604.1; -.
                                                                                                                                                            cell
                                                                                                                                                                      variation in patients with diverse
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                        IPR000777; GP120.
0516; GP120; 1.
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1; -.
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Pred. No. 10;
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Best Local s
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SEQUENCE FROM N.A.
STRAIN=PATIENT A;
MEDLINE=97184515; PubMed=9032317;
McDonald R.A., Mayers D.L., Chung
Birx D.L., Michael N.L.;
                                                                                                                                                        P90085 PRELIMINARY; PKT; 2** ....
P90085, O1-MAY-1997 (TrEMBLIPEL 03, Created)
O1-MAY-1997 (TrEMBLIPEL 03, Last sequence update)
ENVELOPE GLYCOPROTEIN (FRAGMENT).
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                                                                                                             Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae;
NCBI_TaxID=11676;
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Best Local S
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MEDLINE-97184515; PubMed-9032317;
MEDDINE-97184515; PubMed-9032317;
MCDOnald R.A., Mayers D.L., Chung R.C.Y., Wagner K.F., kim S.,
Birx D.L., Michael N.L.;
"Evolution of human immunodeficiency virus type 1 env sequence variation in patients with diverse rates of disease progression J. Virol. 71:1871-1879(1996).
EMBL; US9287; AAC5606.1;
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01-MAY-1997 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
ENVELOPE GLYCOPROTEIN (
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les 8; Conserv
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Viruses; Retroid viruses; Retrovirio
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NON_TER
NON_TER
SEQUENCE
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240 A
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7 (TremBLrel. 03, I
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240 AA;
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26756 MW;
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57.18;
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26720 MW;
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57.18;
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Pred. No. 25;
5; Mismatches
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Last annotation update;
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Pred. No. 25;
                R.C.Y.,
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          Wagner K.F.,
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Best Local S
Matches 8
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ENVELOPE GLYCOPROTEIN (FRAGMENT).
                                                                          P90083;
Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae;
                                                                                                                                                                                                               Envelope protein.
NON_TER 1
NON_TER 240
SEQUENCE 240 AA;
                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-PATIENT A;
MEDITINE-97184515; PubMed-9032317;
MEDOnald R.A., Mayers D.L., Chung R.C.Y., Wagner K.F., kim S.,
Birx D.L., Michael N.L.;
"Evolution of human immunodeficiency virus type 1 env sequence
"Train" in matients with diverse rates of disease progression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local
                                                                                                                                                                                                                                                     InterPro; IPRO(
Pfam; PF00516;
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EMBL; U69284; AAC56603.1; -
                                                                                                                            32 KNCSFN-ITTRLRD
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                                                                                                                                       2 EHCNFNDVTTRLRE 15 ::|:|| :|||:
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NON_TER 1
NON_TER 240
SEQUENCE 240 AA;
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EMBL; U69291; AAC56610.1;
InterPro; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 EHCNFNDVTTRLRE 15
::|:|| :|||||:
32 KNCSFN-ITTRLRD 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                    Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 57.1
8; Conservative
                                                                                                                                                                                                                240
240 AA;
                                                                                                                                                                                                                                                               IPR000777;
                                                                             PRELIMINARY;
                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240
240 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                     GP120; 1.
                                                                                                                                                                                                              240
26747
                                                                                                                             44
                                                                                                                                                                        44.3%;
57.1%;
                                                                                                                                                                                                                                                             GP120.
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26729 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44.3%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                 03, Created)
03, Last sequence up
17, Last annotation
                                                                                                                                                                                                              WW;
                                                                                                                                                            Score 42.5; D
Pred. No. 25;
5; Mismatches
                                                                                                                                                                5
                                                                            PRT;
                                                                                                                                                                                                         B85EA6F749552442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 42.5;
Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4A3C28B659E4993B CRC64;
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                                                                           240
Lentivirus
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                                   update)
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                                                                                                                                                                                                        CRC64;
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                                                                                                                                                         Indels
                                                                                                                                                                          Length
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                                                                                                                                                      1;
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RESOLT Q9S0911 D Q9S0911 D Q9S091 D DT Q9S
                        RESULT
Q9IK02
ID Q9
AC Q9
DT 01
DT 01
DT 01
DT 01
DT 01
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Best Local S
Matches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 8
Q9IK02 PRELIMINARY; PKT; 0/3 cn.
Q9IK02; O1-OCT-2000 (TrEMBLrel. 15, Created)
O1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
O1-UN-2001 (TrEMBLrel. 17, Last annotation update)
TRUNCATED ENVELOPE GLYCOPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9S091;
01-MAY-2000
01-MAY-2000
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Lathigra R., White O., Dodson R., Hickey E.K., Gwinn M., Peterson J., van-Vugt R Palmer N., Haft D., Rosa P., Stevenson B.;
"A bacterial genome in flux: The twelve linear and nine circular extrachromosomal DNAs in an infectious isolate of the Lyme disease spirochete Borrelia burgdorferi.";
Mol. Microbiol. 0:0-0(1999).
EMBL; ABO01579; AAR07613.1; -.
Hypothetical protein; Plasmid.
SEQUENCE 313 AA; 35968 MW; E81A8779733736C5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-PATIENT A;
MEDLIND-97184515; PubMed-9032317;
MCDOnald R.A., Mayers D.L., Chung R.C.Y., Wagner K.F., kim S.,
Birx D.L., Michael N.L.;
Birx D.L., Michael N.L.;
"Evolution of human immunodeficiency virus type 1 env sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       variation in patients with diverse
cell function.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmid cp32-7
Bacteria; Spir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Borrelia burgdorferi (Lyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BB017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9S091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Envelope protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Virol
                                                                                                                                                                                                                                                                                        211
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                                                                                                                                                                                                                                                                                                                                                                                             Similarity 9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 57.3
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Spirochaetales; Spirochaetaceae; Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71:1871-1879(1996).
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0 (TrEMBLrel. 13, Las
0 (TrEMBLrel. 13, Las
AL 36.0 KDA PROTEIN.
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240 AA;
                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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240
26747 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                   44.3%;
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57.1%;
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                          Score 42.5; I
Pred. No. 32;
1; Mismatches
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Pred. No. 25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 313;
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van-Vugt R.,
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                        RESULT
Q73350
ID Q7
AC Q7
DT 01
DT 01
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Q91K06
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Query Match
Best Local
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Best Local :
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EMBL; AF217165; AAF75507.1; -.

InterPro; IPR000328; Env_GP41.

InterPro; IPR000777; GP120.

Pfam; PF00516; GP120; 1.

Pfam; PF00517; GP41; 1.
Q73350
Q73350;
01-NOV-1996
01-NOV-1996
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Q91K06;
Q1-OCT-2000
01-OCT-2000
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                     STRAIN-546HC-B6;
Gartner S., Liu Y., Tang X.P., McArthu
"Analysis of human immunodeficiency vi
a patient with HIV dementia: evidence
brain.";
                                                                                                                                                                                                                                      Pfam; PF00516; GP120; 1.
Pfam; PF00517; GP41; 1.
SEQUENCE 684 AA; 7726
                                                                                                                                                                                                                                                                             J Neurovirol. 0:0-0(2000).
EMBL, PE217161; AAR75503.1; .
Interpro; IPR000328; Env_GP41.
Interpro; IPR000777; GP120.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Human immunodeficiency virus type 1. Viruses; Retroid viruses; Retroviridae; NCBI_TaxID=11676;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gartner S., Liu Y.,
"Analysis of human :
a patient with HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae;
NCBI_TaxID=11676;
[1]
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                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                            153 KNCSFN-ITTRLRD
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                                                                                                                                        2 EHCNFNDVTTRLRE 15
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8; Conserv
                                                                                                                                                                    Similarity
8; Conserv
(TrEMBLrel.
                                          PRELIMINARY;
                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                    GP41; 1.
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                                                                                                                                                                                                                                                                                                                                                                  Tang X.P., McArthur J
immunodeficiency virus
                                                                                                             165
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                                                                                                                                                                               44.38; 57.18;
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Last annotation update)
Created)
Last sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
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Pred. No. 70;
5; Mismatches
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                                                                                                                                                                                 Score 42.5;
Pred. No. 70;
                                           PRT;
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irus type 1 gp160 sequences
for monocyte trafficking ir
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lentivirus
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EMBL; AF217162; AAF75504.1; -

InterPro; IPR000328; Env_GP41.

InterPro; IPR000777; GP120.

Pfam; PF00516; GP120; 1.

Pfam; PF00516; GP41; 1.

SEQUENCE 861 AA; 97808 MW; (
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Best Local
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                                                                                                                    153
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Viruses; Retroid viruses; Retroviridae; Lentivirus
NCBI_TaxID=11676;
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53 KNCSFN-ITTRLRD 165
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SEQUENCE 852 AA; 96383 MW;
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STRAIN-BU/91/07;
MEDLINE-96303593; PubMed-8744585;
Penny M.A., Thomas S.J., Douglas N.W., Ranjbar S.,
Daniels R.S.;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBL_TaxID=11676;
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"Analysis of human ir
a patient with HIV de
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InterPro; IPR000777, GP120.
Pfam; PF00516; GP120, 1.
Pfam; PF00517; GP41; 1.
SEQUENCE 861 AA; 97763 MW;
                                               153 KNCSFN-ITTRLRD
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EMBL; AF217163; AAF75505.1;
                                                                                                                                                                                                                                                                                                                        Q91K04 PRELIMINARY; PRT; 861 AA.
Q91K04; O1-CCT-2000 (TrEMBLrel. 15, Created)
O1-CCT-2000 (TrEMBLrel. 15, Last sequence up
O1-JUN-2001 (TrEMBLrel. 17, Last annotation
ENVELOPE GLYCOPROTEIN.
                                                                                                                                                                                                                                                                                               Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae;
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8; Conservative
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immunodeficiency virus type 1 gp160 sequences from
dementia: evidence for monocyte trafficking into
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Human membrane att	Sequence of the 1F	Human CD59 protein	Human secreted pro	Human secreted pro	Human secreted pro	Human membrane att	Sequence of CD59.	Human lymphocyte s	Human membrane att	Human CD59 protein	Description		ū

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ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CC activity. It provides (i) molecules structurally mimicking human CD59 carbined acid residues 42-58 (region which serves as binding site for CD59 complex interactions) when they are in a spatial orientation which can CC5 specifically bind to amino acid residues 359-384 of human C9. (ii) complex. Compounds that mimicking CD59 amino acids 359-384 when they are in a spatial orientation of the human C5b-9 complex. These mimetics CC in a spatial orientation which can promote the formation of the C5b-9 complex. Complex. Compounds that mimic CD59 can be used to increase CD59 complex. Compounds that mimic CD59 can be used to increase CD59 complex. Compounds that mimic CD59 can be used to increase CD59 complex assembly. This is especially useful in carthritis, scleroderma. Compounds that mimic C9 can be used to promote carthritis, scleroderma. Compounds that mimic C9 can be used to promote carthritis, scleroderma. Compounds that mimic C9 can be used to promote cartivation. The composition can be administered as an adjunct to tumour cantigen) protein fragment.
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Best Local
                               (YAMA ) YAMANOUCHI PHARM CO LTD
                                                                                                                 13-JUN-1996;
                                                                              16-JUN-1995;
                                                                                                                                                                                              WO9700320-A1.
                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; membrane attack complex; inhibitory factor; MACIF; mutant; inhibition; complement; mediation; cytolysis; PGI2; bFGF; basic;
                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                  transplant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human membrane attack complex inhibitory factor mutant Ass18Gln.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW09041;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW09041 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42 fehcnfndvttrlrene 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Compounds modulating CD59 mediated complement activity, treatment of, e.g. immunovasculitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 FEHCNENDVTTRLRENE 17
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17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                          growth factor; suppression; hyperacute; inflammation; rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                      95JP-0174282
                                                                                                           96WO-JP01609
                                                                                                                                                                                                                                                  /label= mat_peptide
                                                                                                                                                                                                             /note= "wild type Asn replaced by {
m Gln}"
                                                                                                                                                                                                                                                                                         /label= sig_peptide 26..102
                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
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Pred. No. 5.3e-08;
Mismatches 0;
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g VΩ

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AAR11426
                          This protein is similar to the murine lymphocyte antigen Ly 6. Antibodies raised against the antigen can be used in formulations for the treatment of autoimmune diseases, cancer and infections.
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Best Local
See also AAQ11252-4
                                                                                                     Claim 1; Page 1; 12pp; Japanese
                                                                                                                                    Surface antigen of human lymphocyte immune system of 101 residues
                                                                                                                                                                                                                                          (TORA ) TORAY IND INC
                                                                                                                                                                                                                                                                             14-JUL-1989;
                                                                                                                                                                                                                                                                                                            14-JUL-1989;
                                                                                                                                                                                                                                                                                                                                               01-MAR-1991.
                                                                                                                                                                                                                                                                                                                                                                           JP03048696-A.
                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human lymphocyte surface antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                            lymphocyte; surface antigen; autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-JUN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR11426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR11426 standard; Protein; 103 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is the human membrane attack complex inhibitory factor (MACIF) mutant Asn18Gln (residues 1-77), which inhibits complement mediated cytolysis, and the release of PGI2 and basic fibroblast growth factor (bFGF) by complement. It can be used to suppress transplanted organ rejection, especially hyperacute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                        corresponding nucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified human membrane attack complex inhibitory factor - has glutamine at position 18 and is an antiinflammatory and complement blocker, useful for inhibition of transplant hyper-acute rejection
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Yamaji N,
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DB; AAQ11251.
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DB; AAT49584.
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17; Conserv
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               sequence does not include an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organ rejection, especially hyperacute the non-lethal effects of complement,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 96; DB 15; Pred. No. 7.1e-08;
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                                                                                                                                               study of
                                                                                                                                                                                                                                                                                                                                                                                                                          cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 102;
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RESULT
AAR80239
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Best Local 9
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Best Local
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                                                                                                                                                                   The inventors claim a cell which contains a gene sequence which encodes protein CD59.CD59 is expressed by the cell and CD59 inhibits complement mediated attack of the cell. The cells fail to elicit T lymphocyte mediated attack or are resistant to complement mediated attack. They can be used to treat patients with immune disorders.
                                                                                                                                                                                                                                                                                                                                              (OKLA-)
                         AAR80239 standard;
                                                                                                                                                                                                                                            express surface proteins encoded by class histocompatability complex genes
                                                                                                                                                                                                                                                              Genetically engineered mammalian cell for treatment of coronary artery disease - inhibits complement-mediated attack and does not
                                                                                                                                                                                                                                                                                        WPI; 1993-058786/07.
N-PSDB; AAQ36708.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-JUN-1993
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                                                                                                                                                     Sequence
                                                                                                                                                                                                                             Claim
                                                                                                                                                                                                                                                                                                                             Bell L,
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29-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                    14-JUL-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9302188-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complement mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence of CD59
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                                                                             1 FEHCNENDVTTRLRENE 17
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                                                                     fehcnfndvttrlrene 58
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17; Conser
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17; Conserv
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                                                                                                                                                                                                                                                                                                                            Bothwell ALM,
                                                                                                                                                                                                                           Page 75;
                                                                                                                                                     103
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                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first
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92US-0906394.
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                                                                                                                                                                                                                                                                                                                   PJ,
                         Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            attack inhibitor;
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                                                                                                                 .08;
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Pred. No.
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Pred. No.
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                                                                                                        Mismatches
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7.2e-08;
                                                                                                                          DB 14;
                                                                                                               .2e-08;
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                                                                                                                        Length 103;
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Matches Query Match Best Local

Similarity 17; Conserv

Conservative

0,

Mismatches

100.0%;

Score 96; Pred. No.

DB 16; . 7.5e-08; ches 0;

Length 107; Indels

0;

Gaps

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21-APR-1989;
12-JUL-1989;
06-SEP-1989;
13-SEP-1989;
                                 Human membrane attack complex inhibition factor (MACIF) regulates the complement system in the final stage of complement activation, and inhibits damage of human cells and tissues as a result of MAC formation. Naturally occuring human MACIF is a glycoprotein of mol. wt. 18 +/- 1 kDa (by SDS-PAGE) with a phosphatidylinositol (PI) anchor at position 76 (Glu) at the C-terminus. When the gene encoding MACIF is expressed in bacteria, the gene (see AAQ98532) gives a modified human MACIF protein comprising 128 amino acid residues (AAR80240); the PI
                                                                                                                                                                                                                                                                     Furuichi I
Yamaji N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MACIF; membrane attack complex inhibition factor; complement system; regulation; activation; final stage; inhibit damage; disease therapy; type II allergy; type III allergy; inflammatory disease treatment; phosphatidylinositol anchor; glycoprotein; diagnosis.
                                                                                                                                                                          Peptide with human membrane attack complex inhibition factor activity - also DNA and expression vectors used to regulate the complement system in the final stage of complement activation
                                                                                                                                                                                                                                N-PSDB;
Sequence
                         anchor attachment does not occur in that case.
                                                                                                                                                      Claim
                                                                                                                                                                                                                                WPI; 1995-321975/42.
N-PSDB; AAQ98532.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Key
                                                                                                                                                                                                                                                                                                          (YAMA ) YAMANOUCHI PHARM CO LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                         19-APR-1990;
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                                                                                                                                                     2; Page 28; 49pp; English.
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  107
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89JP-0103088.
89JP-0179933.
89JP-0230983.
89JP-0238246.
89JP-0247818.
 A
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/note= "optionally not present, r
H or Met"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= PI_anchor
/note= "modified by PI -
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                                                                                                                                                                                                                                                                    Sugita Y,
Yusakawa K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "modified by PI - skeletal structure composed
of phospho-ethanolamine, glycan and
phosphatidylinositol"
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Kasukawa K,
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Takemoto
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RESULT
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Best Local Similarity
Matches 17; Conserv
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                                                                  AAG03765 standard; Protein; 115 AA.
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N-PSDB; AAC03770.
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CC The present sequence is a polypeptide encoded by one of a large number CC of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs CC different tissues. EST sequences usually correspond mainly to the 3' CC untranslated region (UTR) of the mRNA because they are often obtained CC isolating cDNA sequences derived from the 5' ends of mRNAs and even in CC UTR is rarely included. 5' ESTs are derived from the 5' ends of mRNAs and even in CC UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' CC ends and can therefore be used to obtain full length cDNAs and genomic CC chromosome mapping procedures. They are used to obtain upstream cCC regulatory sequences and to design expression and secretion vectors.
Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 13; SEQ ID 7846; 71pp + CD-ROM; English.
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                                                                  protein, SEQ ID NO: 7847.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 96;
Pred. No.
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                                                                                                                                                                                    CD59 mediated complement; human; Cd59 protein; C9 protein; mimetic; tumour therapy; complement-mediated inflammation; immune disorder; immunovasculitis; rheumatoid arthritis; scleroderma; C5b-9 complex;
(BLOO-)
                                                                                                                      W09940115-A2
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                                                                                                                                                                          plasma
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                                                                                                                                                                                                                                                                                                AAY27311;
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                                                                                                                                               Homo sapiens
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DB; AAC03772.
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17; Conser
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BLOOD CENT RES FOUND OKLAHOMA MEDICAL RES
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INC.
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Pred. No.
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8.1e-08;
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cell membrane damage
                                    New glyco:protein 1F5 antigen -
derived from human cell membrane, inhibits complement-mediated
                                                                                                                                                                               WPI; 1990-016630/03.
N-PSDB; AAQ03116, AF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence of the 1F5 antigen derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR04704;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR04704 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          therapy. The present sequence antigen) protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Compounds modulating CD59 mediated complement activity, treatment of, e.g. immunovasculitis % \left( 1\right) =\left\{ 1\right\}                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              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                                                                                                                                                                                                                                                                                                                     Okada
                                                                                                                                                                                                                                                                                                                                                                                                    (MITU)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAY-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-JUL-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EP351313-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human 1F5 antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 1A; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 FEHCNENDVTTRLRENE 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1999-527301/44.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l Similarity
17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                    MITSUBISHI KASEI CORP
                                                                                                                                                                                                                                                                                                                 Okada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                127
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llarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89JP-0172187.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89EP-0401996
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                                                                                                                                                                                    AAN93318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunodiagnosis; pernicious anaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein;
                                                                                                                                                                                                                                                                                                            Nagami Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
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Pred. No. 9e-08;
                                                                                                                                                                                                                                                                                                            Takahashi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from human cell membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20;
                                                                                                                                                                                                                                                                                                                 Takizawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                            Η,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for
                                                                                                                                                                                                                                                                                                                 Kondo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            site for CD59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement
human CD59
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Claim 3; p.

26pp; English.

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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Typically it is prepd. from human erythrocytes which are centrifuged and CC the cell membrane fraction suspended overnight in buffer contg. 1% CC n-octyl-beta-D-glucopyranoside (NOG). After centrifugation, the super-central is treated with solid (NH4)2SO4 to 60% sath. After centrifugation cC with a mol. wt. of 20-25 kD. If contains N-glycoside type carbohydrate cc membrane damage. It may be used to generate polyclonal or cc with as principles (Abs) which may be used to determinine cc lymphocytes or other cells, thus enabling the diagnosis of diseases, cc such as pernicious anaemia, rheumatoid arthritis. CC systemic lupus erythematosus and glomerular nephritis. It may be used to treat disorders in which complement archivation is involved. Abs to it can connect consideration of malignant cells. Residues 27-70 are encoded by the polymerase chain reaction (in AAN93318).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Qy
                    Tomita M, Sı
Yusakawa K,
WPI; 1990-322496/43
                                                                                 27-OCT-1989;
21-APR-1989;
12-JUL-1989;
06-SEP-1989;
13-SEP-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                              (YAMA ) YAMANOUCHI PHARM KK.
                                                                        21-SEP-1989;
                                                                                                                                             19-APR-1990;
                                                                                                                                                                  24-OCT-1990
                                                                                                                                                                                      EP394035-A
                                                                                                                                                                                                                      Protein
                                                                                                                                                                                                                               Key
                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                             Haemolysis; late complement components
                                                                                                                                                                                                                                                                                     Human membrane attack complex inhibition factor (MACIF) gene
                                                                                                                                                                                                                                                                                                                                                       AAR07444 standard; protein; 128
                                                                                                                                                                                                                                                                                                                       28-JAN-1991
                                                                                                                                                                                                                                                                                                                                            AAR07444;
                                                                                                                                                                                                                                                                                                                                                                            444
                                                                                                                                                                                                                                                                                                                                                                                                            67 fehcnfndvttrlrene 83
                                                                                                                                                                                                                                                                                                                                                                                                                        1 FEHCNENDVTTRLRENE 17
                  Sugita Y,
K, Yano S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 100.
17; Conservative
                                                                 89JP-0281197.
89JP-0103088.
89JP-0179933.
89JP-0230983.
89JP-0238246.
89JP-0247818.
                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                         90EP-0304203
                                                                                                                                                                                                                  Location/Qualifiers 26..128
                                                                                                                                                                                               /label≃Mature MACIF protein.
               Takemoto T
Yamaji N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
        o T, Ito ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 96;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                         ΑA
             Furuichi K,
to K;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                           рь
9e-08;
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 11; Length 128;
                    Takayama
                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                    Z
                                                                                                                                                                                                                                                                                                                                                                                                                                           0,
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DR XXX PT PT PT XXX XXX PS XXX SQ
                                             Clone is derived from the Ly-6 cDNA sequence from a human lymphocyte cDNA library. The product may be useful in the study and development of drugs for the treatment of autoimmune diseases and cancer. Probes may also be developed for the isolation of other gene families.
                                          Sequence
                                                                                                       Claim 5; Page 1203; 16pp; Japanese.
                                                                                                                             Surface antigen of human lymphocyte - and gene and antibody useful for investigation and treatment of auto:immune disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                      WPI; 1991-144848/20.
N-PSDB; AAQ11684-6.
                                                                                                                                                                                                    (TORA ) TORAY IND INC
                                                                                                                                                                                                                          23-AUG-1989;
                                                                                                                                                                                                                                               23-AUG-1989;
                                                                                                                                                                                                                                                                   05-APR-1991.
                                                                                                                                                                                                                                                                                      JP03081297-A.
                                                                                                                                                                                                                                                                                                                     Protein
                                                                                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                              Ly-6; cancer; autoimmune disease; pre A precursor.
                                                                                                                                                                                                                                                                                                                                                                                                  Human lymphocyte surface antigen precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                 24-JUL-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR11876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR11876 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene product may be expressed in large quantities and pure form from CHO cells, useful for inhibiting the activity of late complement components ie. haemolysis resulting from MAC formation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 1; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genes encoding protein with human MACIF activity - also expression vectors and proteins produced from expression of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAQ06262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l Similarity
17; Conser
                                        128 AA;
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ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                      89JP-0218183.
                                                                                                                                                                                                                                          89JP-0218183
                                                                                                                                                                                                                                                                                               /label= Mature surface antigen
                                                                                                                                                                                                                                                                                                                   26.
                                                                                                                                                                                                                                                                                                                     /label= Pre A precursor
                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 96; DB 11;
Pred. No. 9e-08;
0; Mismatches 0
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Score Pred.

96; No.

DB 12; 9e-08;

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RESULT 13
AAR80240
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                            Human membrane attack complex inhibition factor (MACIF) regulates the complement system in the final stage of complement activation, and inhibits damage of human cells and tissues as a result of MACI formation. Naturally occuring human MACIF is a glycoprotein of mol. wt. 18 +/- 1 kDa (by SDS-PACE) with a phosphatidylinositol (PI) anchor at position 76 (Glu) at the C-terminus. When the gene encoding MACIF is expressed in bacteria, the gene (see AAQ98532) gives a modified human MACIF protein comprising 128 amino acid residues (AAR80240); the PI
Sequence
                                                                                                                                    Disclosure;
                                                                                                                                                         activity - also DNA and expression vectors used to regulate the complement system in the final stage of complement activation {\sf complement}
                                                                                                                                                                        Peptide with human membrane attack complex inhibition factor activity - also DNA and expression vectors used to require
                                                                                                                                                                                                                                                      Furuichi
                                                                                                                                                                                                                                                                                                             06-SEP-1989;
13-SEP-1989;
                                                                                                                                                                                                                                                                                                                                               27-OCT-1989;
21-APR-1989;
                                                                                                                                                                                                                                                                                                                                                                                 19-APR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               regulation; activation; final stage; inhibit damage; disease thera type II allergy; type III allergy; inflammatory disease treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MACIF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human membrane attack complex inhibition factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR80240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR80240
                                                                                                                                                                                                       N-PSDB; AAQ98532.
                                                                                                                                                                                                                    WPI; 1995-321975/42
                                                                                                                                                                                                                                                                                                                                    12-JUL-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                             EP672683-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   phosphatidylinositol anchor; glycoprotein; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                        20-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                           ramaji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          attachment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17;
                                                                                                                                                                                                                                                                             YAMANOUCHI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard;
 128
                                                                                                                                                                                                                                          Yano S,
                                                                                                                                     Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                    Ito K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                   89JP-0230983.
89JP-0238246.
89JP-0247818.
                                                                                                                                                                                                                                                                                                                                   89JP-0281197.
89JP-0103088.
89JP-0179933.
                                                                                                                                                                                                                                                                                                                                                                                 90EP-0200379
                                                                                                                                     <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label=
26..128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       attack complex inhibition
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "human MACIF" 96..128
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                        does
                                                                                                                                    49pp; English.
                                                                                                                                                                                                                                                                            PHARM CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein;
                                                                                                                                                                                                                                           Yusakawa
                                                                                                                                                                                                                                                     Sugita Y,
                        not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PI_anchor_attachment_signal_sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               secretory_signal_sequence
                      occur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                          ζ,
                                                                                                                                                                                                                                         Takayama M,
Kasukawa K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                        'n
                        that
                      case
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       factor;
                                                                                                                                                                                                                                          Tomita M;
Takemoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement system;
je; disease therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
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Query Match

100.0%;

Score

96;

DВ

16;

Length 128;

Matches

Conservative

0;

Mismatches

0

Indels

0;

Gaps

0

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RESULT 1
AAR86315
               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local
                                                                                                                   Human CD59 (AAR86315) is a terminal complement inhibitor protein (CIP) that includes a C-terminal region involved in directing attachment of a glycosyl-phosphatidylinositol (GPI) anchor. A chimeric transmembrane terminal CIP (TMTCIP) comprising amino acids 1-77 of mature CD59 (i.e. lacking the GPI anchor region) and the transmembrane domain (amino acids 270-350) of human CD46, a membrane cofactor protein. The TMTCIP has been expressed on the cell surfaces of the organs of transgenic animals. Such transgenic organs are protected from human complement attack upon transplantation.
                                                                                                                                                                                                                                                                                                                                            Terminal complement inhibitor chimeric protein and nucleic esp. against human complement, useful for protecting cells complement attack e.g. in organ transplantation
                                                                                     Sequence
                                                                                                                                                                                                                                                                                                          Disclosure; Page 63-64; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1995-320335/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W09523512-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organ transplantation; glycosyl-phosphatidylinositol; GPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Terminal complement inhibitor protein; terminal CIP; CD59; CD46; transmembrane terminal CIP; TMTCIP; Ly6 antigen; transgenic animal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human CD59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR86315;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR86315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rollins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ALEX-) ALEXION PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fehcnfndvttrlrene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEHCNFNDVTTRLRENE
l Similarity
17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        l Similarity
17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                      AAT03338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard;
                                                                                       128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rother RP,
                                                                                       AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94US-0205720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95WO-US02944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= GPI_anchor_region
/note= "GPI anchor region of amino acids 78-103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
1..25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= Ly6 motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .128
               100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Squinto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CD59 protein"
                 .0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
               Score 96; DB 16
Pred. No. 9e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 9e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 corresponds
3 of the matu
                                16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                    Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                 from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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RESULT

15

B Q

67

FEHCNFNDVTTRLRENE

83 17

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RESULT
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                                                               Qy
                                                                                                                                                  This protein sequence comprises human CD59, an inhibitor of complement C55-9 protein. Claimed retroviral vector particles CC express a complement inhibitor such as CD59, and are thereby protected from inactivation upon exposure to body fluids containing CC complement. Also claimed are: (1) a producer cell producing the CC (see also AAW26325) with at least part of the N-terminal receptor-CC (see also AAW26325) with at least part of the N-terminal receptor-CC complement inhibitor activity. The vector is used in a claimed CC method for transducing cells in the presence of a body fluid CC containing complement, preferably ex vivo, especially for gene CC therapy, e.g. of hereditary or acquired blood disorders by containing complement, preferably ex vivo, especially for gene CC transduction of haematopoietic stem cells.
                                                                                     Matches
                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW26318
                                                                                                                                               Sequence
                                        67
                                                                                                                                                                                                                                                                                                                               Disclosure; Column 47-50; 32pp; English.
                                                                                                                                                                                                                                                                                                                                             Retroviral vector particle expressing complement inhibitor activity for transducing cells in body fluids containing complement
                                                                             Local Similarity 100.
hes 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1997-350243/32.
N-PSDB; AAT84472.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Mason
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ALEX-) ALEXION PHARM INC
,16
                                             1 FEHCNENDVTTRLRENE 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUL-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US5643770-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CD59; MACIF; protectin; p18; human; C5b-9 complement inhibitor;
retrovirus; vector; gene therapy; stem cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human CD59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW26318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW26318 standard;
                                fehcnfndvttrlrene 83
                                                                                                                                             128 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Squinto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94US-0278630.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1..25
/label= Sig_peptide
26..128
/label= Mat_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94US-0278630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                            100.0%; S.
100.0%; P
ative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein;
                                                                                        Score 96;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    128
                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A
                                                                                      9e-08;
                                                                                                 DB 18;
                                                                           0
                                                                                             Length 128;
                                                                       Indels
                                                                      0;
                                                                  Gaps
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AAU00685
ID AAU0
XX
AC AAU0
XX
DT 07-S
XX
DE Huma
                                                                                                                                                                                                                                                                               RESULT
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                                                                                                                                                                                     δÃ
                                                                                                                                                                                                                                                                                   CC The sequence represents human CD59 protein which is fused to human or CC porcine CTLA4 protein to form CTLA4-CD59 chimeric protein. Chimeric CC proteins comprising a domain having C5b-9 and/or C3 inhibitory activity CC (e.g. CTLA4) and a domain having T-cell inhibitory activity (e.g. CD59) CC immune responses. These polypeptides and their associated nucleic acids CC immune responses. These polypeptides and their associated nucleic acids CC thumoral and cellular rejection after xenotransplantation into humans. The CC sequences are capable of conferring resistance to humoral and cellular CC mechanisms of immune attack, to protect against human serum complement CC and to inhibit T-cell activation. Transgenic animals (for example, CC e.g. pig, goat, sheep) expressing such a chimeric protein on the surfaces of their cells would have a higher chance of survival.
                                                                                                                                                                                                                           Query Match
Best Local (
                                                                                                                                                                                                               Matches
Human CTLA4-human CD59 chimeric protein.
                            07-SEP-2001 (first entry)
                                                                                         AAU00685
                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                    17
                                                                                                                                                    67 fehcnfndvttrlrene 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Fig 2E(2); 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chimeric protein useful for protecting xenotransplanted tissues by inhibiting cellular both humoral and immune responses, comprises a C5b-9 and/or C3 inhibitory domain, and a T-cell inhibitory domain.
                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAS00682
                                                                                                                                                                 1 FEHCNENDVTTRLRENE 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-300497/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fodor WL, Pizzolato M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-OCT-2000; 2000WO-US29151.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ALEX-) ALEXION PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTLA4; CD59; human; pig; T-cell activation; C5b-9 inhibitory activity; c3 inhibitory activity; cellular immune response; xenotransplantation; humoral immune response; human serum complement; rodent; mouse; rabbit, rat; lagomorph; hare; ungulate; goat; sheep.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200130966-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human CD59 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU00688;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU00688 standard; Protein; 128
                                                                                                                                                                                                          l Similarity
                                                                                standard; Protein; 260 AA.
                                                                                                                                                                                                                                                                              128 AA;
                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0161186
                                                                                                                                                                                                                    100.0%;
                                                                                                                                                                                                          0;
                                                                                                                                                                                                               Score 96; DB 22
Pred. No. 9e-08;
                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A
                                                                                                                                                                                                                              DB 22;
                                                                                                                                                                                                    0
                                                                                                                                                                                                                           Length 128;
                                                                                                                                                                                                  Indels
                                                                                                                                                                                                0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             CC The sequence represents a CTLA4-CD59 chimeric protein, formed from human CC CTLA4 protein and human CD59 protein. Chimeric proteins comprising a C domain having C5b-9 and/or C3 inhibitory activity (e.g. CTLA4) and a C domain having T-cell inhibitory activity (e.g. CD59) are capable of inhibiting both cellular immune responses and humoral immune responses. These polypeptides and their associated nucleic acids are useful for protecting pig cells of tissues and organs from both humoral and cellular capable of conferring resistance to humoral and cellular mechanisms of immune attack, to protect against human serum complement and to inhibit T-cell activation. Transgenic animals (for example, rodents, e.g. mouse, capable of capable, e.g. rabbit, hare; and ungulates, e.g. pig, goat, sheep) capacity activation activation on the surfaces of their cells would be a higher chance of survival.
                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTLA4; CD59; human; pig; T-cell activation; C5b-9 inhibitory activity; C3 inhibitory activity; cellular immune response; xenotransplantation; humoral immune response; human serum complement; rodent; mouse; rabbit
 Chimeric -
                                        CTLA4; CD59; human; pig; T-cell activation; C5b-9 inhibitory activity; C3 inhibitory activity; cellular immune response; xenotransplantation; humoral immune response; human serum complement; rodent; mouse; rabbit
                                                                                                                                              07-SEP-2001
                                                                                                                                                                                                             AAU00684 standard; Protein; 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  inhibiting cellular both humoral and immune responses, comprises a C5b-9 and/or C3 inhibitory domain, and a T-cell inhibitory domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chimeric protein useful for protecting xenotransplanted tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W0200130966-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Fig 2B(2); 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fodor WL, Pizzolato M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-OCT-2000; 2000WO-US29151.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-MAY-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ALEX-) ALEXION PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-OCT-1999;
                                                                                                                                                                                                                                                                                             199
                                                                                                                                                                                                                                                                                                                         \vdash
                                                                                                                                                                                                                                                                                                            FEHCNFNDVTTRLRENE
                              lagomorph;
                                                                                                                                                                                                                                                                                           fehcnfndvttrlrene 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lagomorph; hare; ungulate; goat; sheep; mutant; mutein.
                                                                                                          CTLA4-human CD59 chimeric protein.
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                             260 AA;
                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0161186.
                                hare;
                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                              ungulate;
                                                                                                                                                                                                                                                                                                                         17
                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                         Score 96; DB 22;
Pred. No. 1.9e-07;
                                                                                                                                                                                                               A
                            goat; sheep; mutant;
                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                        Length 260;
                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rabbit;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a
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Search completed: Job time: 32 sec

April

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2002, 10:44:27

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QΥ
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                                                               Query Match
Best Local S
Matches 17
                                                                                                                                                                                 The sequence represents a CTLA4-CD59 chimeric protein, formed from porcine CTLA4 protein and human CD59 protein. Chimeric proteins comprising a domain having C55-9 and/or C3 inhibitory activity (e.g. CTLA4) and a domain having T-cell inhibitory activity (e.g. CD59) are capable of inhibiting both cellular immune responses and humoral immune responses. These polypeptides and their associated nucleic acids are useful for protecting pig cells of tissues and organs from both humoral and cellular rejection after xenotransplantation into humans. The sequences are capable of conferring resistance to humoral and cellular mechanisms of immune attack, to protect against human serum complement and to inhibit T-cell activation. Transgenic animals (for example, rodents, e.g. mouse, rat; lagomorphs, e.g. rabbit, hare; and ungulates, e.g. pig, goat, sheep) expressing such a chimeric protein on the surfaces of their cells would have a higher chance of survival.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chimeric protein useful for protecting xenotransplanted tissues by inhibiting cellular both humoral and immune responses, comprises a C5b-9 and/or C3 inhibitory domain, and a T-cell inhibitory domain
                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 3; Fig 2A(2); 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-300497/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-OCT-2000;
                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fodor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ALEX-) ALEXION PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200130966-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric -
200 fehcnfndvttrlrene
                                 1 FEHCNFNDVTTRLRENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WL,
                                                                   l Similarity
17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAS00678.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pizzolato
                                                                                                                                                       261 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sus scrofa.
                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000WO-US29151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0161186
                                                                                 100.0%;
                                                                   0;
                                                                                   Score 96; DB 22;
Pred. No. 1.9e-07;
                                                                 Mismatches
                                                                   0;
                                                                                               Length
                                                                   Indels
                                                                                                     261;
                                                                   0,
                                                                   Gaps
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OM protein - protein search, using sw model
                                                                                                                                                                                                               Result
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Searched
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     987654
                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                             Score
     999999999
                                                                                                                                                                                           Query
Match
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16:
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  April 2, 2002, 09:19:51; Search time 93.32 Seconds (without alignments) 50.580 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3148936 seqs, 277657034 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-020-393B-3_COPY_42_58
96
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(cgn2_6/ptodata/2/paa/US085_COMB.pep: *

(cgn2_6/ptodata/2/paa/US085_COMB.pep: *

(cgn2_6/ptodata/2/paa/US086_COMB.pep: *

(cgn2_6/ptodata/2/paa/US086_COMB.pep: *

(cgn2_6/ptodata/2/paa/US089_COMB.pep: *

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(cgn2_6/ptodata/2/paa/US099_COMB.pep: *

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/cgn2_6/ptodata/2/paa/US06_COMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cgn2_6/ptodata/2/paa/US082_COMB.pep:*
/cgn2_6/ptodata/2/paa/US083_COMB.pep:*
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/cgn2_6/ptodata/2/paa/US080_COMB.pep:*
/cgn2_6/ptodata/2/paa/US081_COMB.pep:*
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   70
77
80
103
103
103
122
122
122
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24
13 US-08-952-333C-28

14 US-09-020-393B-3

15 US-08-043-446A-6

15 US-07-906-394-3

15 US-08-021-602-3

15 US-08-086-549-3

17 US-09-086-549-3

18 US-09-086-34-366-13482

18 US-09-020-393B-1
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Compugen Ltd
Sequence 28, Appli
Sequence 3, Appli
Sequence 6, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 13482, A
Sequence 13482, A
Sequence 1, Appli
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ALIGNMENTS

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RESULT 1
US-08-952-333C-28
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/952,333C
FILING DATE: 17 FEBRUARY 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/NL95/00169
FILING DATE: 10 MAY 1995
                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Brakenhoff, Rudolf Henrikus; Van Dongen, Augustina APPLICANT: Antonius Maria Sylvester TITLE OF INVENTION: Methods for detection and therapy....epitopes TITLE OF INVENTION: and antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                 STREET: 767 Thi
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                         COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                    10017
                                                                                                                                                                                                                                                                                                                                 New York
                                                                                                                                                                                                                                                                                                                                                                                   767 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                              Frischauf Holtz Goodman Langer and Chick
                                                                                                                                                                                                                                Floppy disk
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Appli

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ORGANISM: 08-09-020-393B-3
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                                                                                                                                                                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/020,3931
FILING DATE: 03-FEB-1998
CLASSIFICATION: 514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qy
                                                                                                                                                   CLASSIF TOATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION UNMEER: 31,284
REFERENCE/DOCKET NUMBER: OMRE
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-873-8794
                                                                                                               TELEFAX: 404-873-8795
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-952-333C-28
                       MOLECULE TYPE: PO
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 28180
REFERENCE/DOCKET NUMBER: 9706
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 319-4900
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 77 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Compositions and Methods to Inhibit the
                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                              STREET: St.
CITY: Atlanta
STATE: GA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Barth, Richard S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42 FEHCNFNDVTTRLRENE 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Match
Local Similarity 100.0%; Score 96;
Local Similarity 100.0%; Pred. No.
hes 17; Conservative 0; Mismatc)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 FEHCNENDVTTRLRENE 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 70 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                              30309-3450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/09020393B
                                                                                                                                                                                                                                                                                                                                                                                          GA
             Human
                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sims, Peter J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HCD59 fragment of figure 5
                                                 peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown
                                                                                                                                                                                                                                                                                  Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.2e-08;
ches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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RESULT 4
US-07-906-394-3
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TOPOLOGY: line
MOLECULE TYPE: US-08-043-446A-6
                                                                                                              Sequence 3, Application:
                                                                                                                                                                                                                                                   Ouery Match 100.0%; Score 96; DB 4; I Best Local Similarity 100.0%; Pred. No. 8.4e-08; Matches 17; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-043-446A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPOTER REALABLE FORM.

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatable
OPERATING SYSTEM: PC CONS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/043,446;
FILING DATE: 05-APR-1993
CLASSIFICATION: 435
AMPROBMENT ACCOUNT TWENDMARTAN.
                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin p.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX03*
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 415-496-1200 INFORMATION FOR SEQ ID NO:
                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/08043446A GENERAL INFORMATION:
                                     APPLICANT:
                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 80 amino acids
TYPE: amino acid
CTDANITEDATEO ACID
                                                                                                                                                                                                      51 FEHCNFNDVTTRLRENE 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Boyd, Richard L.
APPLICANT: Godfrey, Dale I.
APPLICANT: MacNell, Ian A.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: MAMMALIAN DEVELOPMENTAL ANTIGENS
                                                                                                                                                                                                                      1 FEHCNFNDVTTRLRENE 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATY: Palo Alto
STATE: California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42 FEHCNFNDVTTRLRENE 58
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                                                                                                                             Application US/07906394
          Madri, Joseph
Rollins, Scott
Bell, Leonard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94304-1104
                                                  Bothwell, Alfred L.I
Elliott, Eileen A.
Flavell, Richard A.
Squinto, Stephen
                                                                                                     Sims, Peter J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                    linear
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                                                                                                                                                                                                                                                                                                                                                    protein
                                                                                                                                                                                                                                                                                                                                                                             single
                                                                                    Alfred L.M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Release #1.0, Version #1.25
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 14; Length 77;
                                                                                                                                                                                                                                                                              Length 80;
                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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TITLE OF INVENTION: UT NUMBER OF SEQUENCES: 4

ADDRESSEE:

CITY: Atlanta

1100 Peachtree Street, Suite 2800

Kilpatrick & Cody

Universal Donor Cells

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B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      us-07-906-394-3
                                                                                                                                                                                                                                                                            Sequence 3, Application US/08021602
GENERAL INFORMATION:
APPLICANT: Fodor, William L.
APPLICANT: Fodor, William L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                       TITLE OF INVENTION: Transcriptional Cassette
TITLE OF INVENTION: for the Expression of Complement Regulatory
TITLE OF INVENTION: Proteins in Transgenic Animals
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: CD59
                                               ZIP: 06430
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 103 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,7
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 404-815-6500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
MEDIUM TYPE: 3.5 inch, 760 Kb storage
COMPUTER: DELL 486/50
OPERATING SYSTEM: DOS 5.0
SOFTWARE: Displaywrite 5
                                                                                                                                       STREET: 1951 Bu
CITY: Fairfield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US
FILING DATE: 19920629
                                                                                                      COUNTRY:
                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                           42 FEHCNFNDVTTRLRENE 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 FEHCNFNDVTTRLRENE 17
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17; Conserv
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                                                                                                                                                                                                                                                                                                                                   Application US/08021602
                                                                                                                         Connecticut
                                                                                                                                                        1951 Burr Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                103 amino acids
                                                                                                        USA
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                                                                                                                                                                          Maurice M. Klee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-terminal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 96; DB 3; 100.0%; Pred. No. 1.1e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31,284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 103;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (203) 254 110 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYPOTHETICAL: NO ANTI-SENSE: NO FRAGMENT TYPE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
TOPOLOGY: lin
MOLECULE TYPE:
                                                                                          COUNTRY: U.S.
ZIP: 30309-4530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMMEDIATE SOURCE:
CLONE: CD59
                                                                                                                                                                                                                                                                   ADDRESSEE: Kilpatrick & Cody
                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                                                                                     STREET: 1100 P
CITY: Atlanta
STATE: Georgia
                                                                                                                                                                                                                                                                                                                      TITLE OF
                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Klee, Maurice M. REGISTRATION NUMBER: 30 REFERENCE/DOCKET NUMBER:
                                                              APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: UPFILING DATE: 19930222
                                                 CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                   I: Squinto, Stephen
INVENTION: Universal Donor Cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/08086549
                                                                                                                                                                                                                     Georgia
                                                                                                                                                                                                                                                      1100 Peachtree Street, Suite 2800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          103 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                               Bothwell, Alfred L.M. Elliott, Eileen A. Flavell, Richard A.
                                                                                                                                                                                                                                                                                                                                                                                Madri, Joseph
                                                                                                                                                                                                                                                                                                                                                  Bell, Leonard
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linear
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) 254 1101
) ID NO: 3:
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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REFERENCE/DOCKET NUMBER: OM TELECOMMUNICATION INFORMATION: TELEPHONE: 404-815-6500

OMRF135

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APPLICANT: Bejanin, Stephane
APPLICANT: Tanaka, Hiroaki
APPLICANT: Dumas Milne Edwards, Jean Baptiste
APPLICANT: Jobert, Severin
APPLICANT: Jobert, Severin
APPLICANT: Giordano, Jean-Yves
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: 81. US2. REG
CURRENT APPLICATION NUMBER: US/09/834,366
CURRENT FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: US 60/197,873
NUMBER OF SEO ID NOS: 52153
SOFTWARE: Patent.pm
SOFTWARE: Patent.pm
TYPE: PRT
OBSANTON. Homo serions
                                                                            RESULT 8
US-60-197-873-13482
                                                                                                                                                               Query Match
Best Local Similarity luv.v.
Watches 17; Conservative
                                                                                                                                         В
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                                            Sequence 13482, Application US/60197873 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 7
US-09-834-366-13482
/ Sequence 13482, Application US/09834366
/ GENERAL INFORMATION:
                            APPLICANT:
              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Дb
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Best Local
                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGINAL HOME ORGANISM: HOME IMMEDIATE SOURCE:
                                                                                                                            TELEFAX: 404-813-033:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 103 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL: NO ANTI-SENSE: NO FRAGMENT TYPE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42 FEHCNFNDVTTRLRENE 58
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hes 17; Conservation
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TYPE: amino acid
STRANDEDNESS: sing
TOPOLOGY: linear
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Dumas Milne Edwards, Jean Baptiste
                        Bejanin, Stephane
Tanaka, Hiroaki
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100.0%; F
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Pred. No. 1
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Pred. No. 1.1e-07;
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                                                                                                                                                                                               Length 122;
                                                                                                                                                                      Indels
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...ruICANT: Jobert, Severin
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: 81.US1.PRO
CURRENT APPLICATION NUMBER: US/60/197,873
CURRENT FILING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 52153
SOFTWARE: Patent.pm
SEQ ID NO 13482
TYPE: PAT
CORGANICATION
CONTROL OF SEQ ID NOS: 52153
US-09-020-393B-1
                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGIZTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRE
TELECOMMUNICATION INFORMATION:
TELEPAN: 404-873-8794
INFORMATION FOR SEQ ID NO: 1:
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NAME/KEY: SIGNAL

LOCATION: -20..-1

US-60-197-873-13482
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US-09-020-393B-1
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Best Local Similarity
Watches 17; Conserve
                          MOLECULE TYPE: I
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/09020393B
GENERAL INFORMATION:
APPLICANT: Sims, Peter J.
TITLE OF INVENTION: Compositions and Methods to Inhibit the
TITLE OF INVENTION: C5b-9 Complex of Complement
NUMBER OF SEQUENCES: 18
                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
                                                                                                                                                                                                                                                                                OPERALLING CONTROL PATENTIN Release #1.0, CURRENT APPLICATION DATA:

CURRENT APPLICATION NUMBER: US/09/020,393B
                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                   TYPE: amino acid
STRANDEDNESS: si
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 2800 OF STREET: St. CITY: Atlanta STATE: GA
                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 03-FEI CLASSIFICATION: 51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 30309-3450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
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    Patrea L. Pabst
2800 One Atlantic Center, 1201 W. Peachtree

                                       . peptide
                                                                                                                                                                                                                                                                                                                                    E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                      03-FEB-1998
N: 514
                                                                                   single
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Pred. No. 1.3e-07;
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; LOCATION: -20..-1
US-09-834-366-18052
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Best Local S
Matches 17
Query Match
Best Local Similarity
                                                                                                                                                                   NUMBER OF SEQ ID NOS:
SOFTWARE: Patent.pm
SEQ ID NO 18056
LENGTH: 128
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SEQ ID NO 18052
LENGTH: 128
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                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: ESTs and Encoded Human Proteins. FILE REFERENCE: 81.US2.REG CURRENT APPLICATION NUMBER: US/09/834,366
                                                                                                                                                                                                                                                                                                                                     APPLICANT: Bejanin, Stephane
APPLICANT: Tanaka, Hiroaki
APPLICANT: Dumas Milne Edwards, Jean Baptiste
APPLICANT: Jobert, Severin
APPLICANT: Giordano, Jean-Yves
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/197,873 PRIOR FILING DATE: 2000-04-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 2001-04-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Bejanin, Stephane
APPLICANT: Tanaka, Hiroaki
APPLICANT: Dumas Milne Edwards, Jean Baptiste
                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/197,873 PRIOR FILING DATE: 2000-04-18
                                                                                                                                                                                                                                                                          CURRENT FILING DATE: \ 2001-04-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 52153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Giordano, Jean-Yves
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: ESTs and Encoded Human Proteins FILE REFERENCE: 81.US2.REG
                                                                                  NAME/KEY: SIGNAL LOCATION: -20. -1
                                                                                                                                  ORGANISM: Homo sapiens
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                                                                                                                       FEATURE:
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17; Conser
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100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 96; DB 22; Length 128; 100.0%; Pred. No. 1.4e-07;
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Score
Pred.
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96;
DB 22;
1.4e-07;
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               Length 128;
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; NAME/KEY: SIGNAL
; LOCATION: -20..-1
US-60-197-873-18052
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; LOCATION: -20..-1
US-09-834-366-18064
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APPLICANT: Tanaka, Hir
APPLICANT: Dumas Milne
APPLICANT: Jobert, Sev
APPLICANT: Giordano, J
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SEQ ID NO 18052
LENGTH: 128
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LENGTH: 128
                                             Query Match
Best Local
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APPLICANT: Tanaka, Hiroaki
APPLICANT: Dumas Milne Edwards, Jean Baptiste
APPLICANT: Jobert, Severin
APPLICANT: Giordano, Jean Yves
TITLE OF INVENNTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: 81.US2.REG
                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/60/197,873 CURRENT FILING DATE: 2000-04-18
                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 52153
SOFTWARE: Patent.pm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/834,366
CURRENT FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: US 60/197,873
PRIOR FILING DATE: 2000-04-18
                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                                       TYPE: PRT
                                                                                                                                                        FEATURE:
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1 FEHCNFNDVTTRLRENE 17
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17; Conserv
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Tanaka, Hiroaki
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                                Conservative
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                                                                                                                                                                                                                                                                                                              ESTs and Encoded Human Proteins
                                                                                                                                                                                                                                                                                                                               Jean-Yves
                              100.0%; Score 96; DB 24; 100.0%; Pred. No. 1.4e-07; ... Mismatches 0;
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                                                             Length 128;
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US-60-197-873-18056

GENERAL INFORMATION: Sequence 18056,

Application US/60197873

APPLICANT: APPLICANT: APPLICANT:

Tanaka,

Bejanin, Stephane

Dumas Milne Edwards, Jean Baptiste Jobert, Severin

В

FEHCNFNDVTTRLRENE

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APPLICANT: Tanaka, Hirorkii
APPLICANT: Dumas Milne Edwards, Jean Baptiste
APPLICANT: Jobert, Severin
APPLICANT: Glordano, Jean-Yves
FILE REFERENCE: 81.US1.PRO
CURRENT APPLICATION NUMBER: US/60/197,873
NUMBER OF SEQ ID NOS: 52153
SEQ ID NO 18064
LENCTH: 128
TYPE: PRT
  RESULT
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                                                            Qγ
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TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: 81.US1.PRO
CURRENT APPLICATION NUMBER: US/60/197,873
CURRENT FILING DATE: 2000-04-18
SOFTWARE: Patent.pm
SEQ ID NOS: 52153
SEQ ID NO 18056
LENGTH: 128
                                                                                    Matches
                                                                                                         Query Match
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                                                                                                                                                          FEATURE:
NAME/KEY: SIGNAL
LOCATION: -20..-1
                                                                                                                                                                                       ORGANISM: Homo sapiens
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Best Local
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NAME/KEY: SIGNAL
NAMTON: -20...-1
                             67 FEHCNFNDVTTRLRENE 83
16
                                         1 FEHCNFNDVTTRLRENE 17
                                                                                               Local
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les 17; Conserv
                                                                                   17;
                                                                                           Similarity
                                                               100.0%; Score 96; DB 24; Length 128; Conservative 0; Mismatches 0; Indels
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Tanaka, Hiroaki
                                                                                                                                                                                                                                                                                                                                                                                      Application US/60197873
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                                                                 0;
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RESULT 18
US-60-160-189-7836
; Sequence 7816, Application US/60160189
; GENERAL INFORMATION:
; APPLICANT: BONAZZI, VIVIEN
; TITLE OF INVENTION: ISOLATED HUMAN DRUG TARGET PROTEINS,
; TITLE OF INVENTION: MUCLEIC ACID MOLECULES ENCODING HUMAN DRUG TARGET PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
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                                                                                                                                                                                                                                                                                                                                 NAME/KEY: VARIANT
LOCATION: (1)...(78)
OTHER INFORMATION: Xaa = Any Amino
US-60-169-840-6378
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US-60-169-840-6378
                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6378, Application US/60169840
GENERAL INFORMATION:
APPLICANT: BONZZZI, VIVIEN
TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: UCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CLO00164
FULE REFERENCE: CLO00164
CURRENT APPLICATION NUMBER: US/60/169,840
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Best Local
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SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO.6378
LENGTH: 78
TYPE: PRT
ORGANISM: Human
FEATURE:
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ORGANISM: HUMAN
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(78)
OTHER INFORMATION: Xaa = Any Amino Acid
US-60-160-203-4361
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Best Local &
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TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CLOO116
CURRENT APPLICATION UMBER: US/60/160,203
NUMBER OF SEQ ID NOS: 6374
SOCTWARE: FastSEQ for Windows Version 4.0
LENGTH: 78
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GENERAL INFORMATION:
                                                                                                                                                                                    17 FEHCNFXDVTTRLRENE 33
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                                                                                                                                                                                                                                                   Local Similarity 94.1
les 16; Conservative
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nes 16; Conserv
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94.18;
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94.18;
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Pred. No. 1.2e.
0; Mismatches
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1,2e-06;
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; NAME/KEY: VARIANT; LOCATION: (1)...(73); OTHER INFORMATION: Xaa - Any Amino Acid US-60-169-867-5425
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COTHER INFORMATION: Xaa = US-60-160-189-7836
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                                                                                                                                                                                                                                                               RESULT 20
PCT-US01-00663-30608
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CURRENT FILING DATE: 1999-12-09
NUMBER OF SEQ ID NOS: 8230
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 5425
LENGTH: 73
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GENERAL INFORMATION:
APPLICANT: Bonazzi, Vivien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/60/160,189
CURRENT FILING DATE: 1999-10-19
NUMBER OF SEO ID NOS: 10162
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 7836
LENGTH: 73
TYPE: PRT
                                                                                                                                                                                                                         Sequence 30608, Application PC/TUS0100663 GENERAL INFORMATION:
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APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: HOMAN GENOME-DERIVED SINGLE EXPRESSION IN HUMAN PLACENTA
FILE REFERENCE: PB 0004 WO 7
CURRENT APPLICATION NUMBER: PCT/US01/00663
CURRENT FILING DAVE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/180,312
                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN DRUG TARGET PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000160
                                                                                                                                                               APPLICANT: Molecular Dynamics, Inc. APPLICANT: Penn, Sharron G. APPLICANT: Rank, David R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
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nes 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                               75.5%;
83.3%;
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Pred. No. 0.00056;
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Pred. No. 0.00056;
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LENGTH: 58
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Best Local Similarity
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PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 27 September 2000 (27.09.00)
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 21 September 2000 (21.09.00)
PRIOR FILING DATE: 12 September 2000 (21.09.00)
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 30 June 2000 (30.06.00)
NUMBER OF SEO ID NOS: 38837
                                                                                                                                                                                    PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
DBIOR STILL CATTON NUMBER: US 60/236,359
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PRIOR FILING DATE: 03 August 2000 (03.08.00)
PRIOR APPLICATION NUMBER: GB 24263.6
                                                                PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
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PRIOR
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PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: AGOMICA-X-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Penn, Sharron G. APPLICANT: Rank, David R.
                                                PRIOR FILING DATE:
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OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL - 16
OTHER INFORMATION: ESTHUMAN HIT: AU139072.1, EVALUE 7.00e-29
OTHER INFORMATION: SWISSPROT HIT: P13987, EVALUE 6.00e-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens FEATURE:
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                                                                                                                                          APPLICATION NUMBER: PCT/US01/00669 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
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Hanzel, David K.
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NUMBER: PCT/US01/00663; 2001-01-30
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26 May 2000
                                           2001-01-30
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100.0%;
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Pred. No.
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0.0024;
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OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 4.6
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 5.6
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 5.6
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.2
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.6
OTHER INFORMATION: EXPRESSED IN HBLLOO, SIGNAL = 5.7
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 5.7
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 6.6
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 5.9
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 5.9
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 7.9
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 5.6
OTHER INFORMATION: SWISSPROT HIT: AU139072.1, EVALUE 7.00e-29
US-09-864-761-37475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-60-236-359-19739
; Sequence 19739, Application US/60236359
; GENERAL INFORMATION:
CONTINUE OF THE INFORMATION: MAP TO AL049629.14

OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 4.6

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 5.6

OTHER INFORMATION: EXPRESSED IN BALIN, SIGNAL = 5.2

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.6

OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 4.6

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.6
                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/60/236,359
CURRENT FILING DATE: 2000-09-27
PRIOR APPLICATION UNUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 21709
SOFTWARE: Molecular Dynamics Sequence Listing Engine
SEQ ID NO 19739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR FILE REFERENCE: MDhMORF-4P
FILE REFERENCE: MDhMORF-4P
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Best Local Similarity 100.
Conservative
                                                                                                                                                                                                                                                         LENGTH: 58
TYPE: PRT
ORGANISM: Homo sapiens
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR APPLICATION NUMBER: US 09/774,203
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 37475
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PRIOR FILING DATE: 2001-01-30
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. 0.0024;
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TELEPHONE: 404-8/3-8795
TELEFAX: 404-873-8795
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
FRIGHH: 75 amino acids
                                                                     Query Match
Best Local Similarity
                                                                Matches
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                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                              ATTORNEY AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31.284
REFERENCE/DOCKET NUMBER: OMFE
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-773-8794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Qy
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OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 5.9
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 7.9
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 5.6
OTHER INFORMATION: EXT. HUMAN HIT: AW374176.1, EVALUE 4.00e-29
US-60-236-359-19739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/09020393B
GENERAL INFORMATION:
APPLICANT: Sims, Peter J.
                                                                                                                                                              HYPOTHETICAL: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
42 FANCNFNDISTLLKENE
                        1 FEHCNFNDVTTRLRENE 17
                                                                                                                                                   ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Compositions and Methods to Inhibit the NUMBER OF SEQUENCES: 18
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OTHER
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STREET: St.
CITY: Atlanta
STATE: GA
                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 03-FEI CLASSIFICATION: 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 30309-3450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
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R INFORMATION:
R INFORMATION:
R INFORMATION:
R INFORMATION:
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13; Conserv
                                                       Conservative
                                                                                                                                                Baboon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3: Patrea L. Pabst
2800 One Atlantic Center, 1201 W. Peachtree
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                     70.8%;
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                                               Score 68; DB
Pred. No. 0.00
4; Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                             170
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                                                               DB 14;
0.0032;
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0.0024;
thes 0; Indels
                                                                        Length 75;
                                              Indels
                                           0;
                                        Gaps
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Sequence 5, Application US/09020393B GENERAL INFORMATION:
APPLICANT: Sims, Peter J.

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PCT-US01-14827-9833
; Sequence 9833, Application PC/TUS0114827
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-104
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US-09-020-393B-5
                                                                                                NUMBER OF SEQ ID NOS: 16102
SOFTWARE: Custom
SEQ ID NO 9833
LENGTH: 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 10; Conserv
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ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/09/020,393B
FILING DATE: 03-FEB-1998
CLASSIFICATION: 514
                                                                                                                                                                            CURRENT APPLICATION NUMBER: PCT/US01/14827
CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 09/577,408
PRIOR FILING DATE: 2000-05-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRE
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-873-8794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 404-873-8795 INFORMATION FOR SEQ ID NO:
                                                         TYPE: PRT
ORGANISM: Homo sapiens
NAME/KEY: DOMAIN
LOCATION: (43)..(52)
                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide HYPOTHETICAL: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Compositions and Methods to Inhibit the TITLE OF INVENTION: C5b-9 Complex of Complement NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 2800 One Atlantic Center, STREET: St. St. CITY: Atlanta
STATE: GA
                                                                                                                                                                                                                                                                                                                                                                                                                                     42 FANCNFNDISTLLKESE 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: si
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  African green monkey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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Pred. No. 0.022;
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Query Match
Best Local Similarity
Matches 8; Conserva
Search completed: April Job time: 171 sec
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                                                                                                                                                                                                                                                                           OTHER INFORMATION: Ly-6 / u-PAR domain proteins domain identified by eMATRIX, OTHER INFORMATION: accession number BL00983A, p-value=7.480e-09, raw score of 5.8 NAME/KEY: DOMAIN LOCATION: (32)..(160) OTHER INFORMATION: u-PAR/Ly-6 domain identified by PFam, accession name OTHER INFORMATION: UPAR_LY6, E-value=7.7e-06, PFam score of 25.4 NAME/KEY: misc_feature LOCATION: (1)...(211) OTHER INFORMATION: Xaa = X or * as defined in Table 2.
                                                                                            103 FEHCNFND 110
                                                                                                                               1 FEHCNFND 8
                                                                                                                                                                     Conservative
                     2
                                                                                                                                                                                        54.2%; Score 52;
100.0%; Pred. No.
                       2002, 09:22:42
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                                                                                                                                                                       Mismatches
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4.4;
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Result
No.
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Maximum Match 100%
Listing first 50 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Searched:
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     DB seq length: 0
DB seq length: 2000000000
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41.5
41.5
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                                       Query
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96
1 FEHCNFNDVTTRLRENE 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                          /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:*
/cgn2_6/ptodata/1.paa/US06_NEW_COMB.pep:*
/cgn2_6/ptodata/1.paa/US07_NEW_COMB.pep:*
/cgn2_6/ptodata/1.paa/US08_NEW_COMB.pep:*
/cgn2_6/ptodata/1.paa/US09_NEW_COMB.pep:*
/cgn2_6/ptodata/1.paa/US09_NEW_COMB.pep:*
/cgn2_6/ptodata/1.paa/US09_NEW_COMB.pep:*
/cgn2_6/ptodata/1.paa/US00_NEW_COMB.pep:*
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US-09-612-314-39
US-09-612-314-42
US-09-612-314-41
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US-09-612-314-43
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US-09-612-314-43
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US-09-612-314-43
US-09-612-314-43
US-09-91-630-12
US-09-91-630-12
US-09-91-630-12
US-09-905-129-15
US-09-905-129-15
US-09-905-129-15
US-09-708-427-16838
US-09-708-427-16837
US-09-708-427-15837
US-09-708-427-56000
US-09-708-427-55099
PCT-US02-0392-531
US-09-708-427-55099
PCT-US02-0392-7381
US-10-032-585-7381
US-10-032-585-7381
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Compugen Ltd
           Sequence 39, Appl
Sequence 41, Appl
Sequence 40, Appl
Sequence 41, Appl
Sequence 43, Appl
Sequence 44, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 16838, A
Sequence 16837, A
Sequence 1695, Appl
Sequence 171, Appl
Sequence 171, Appl
Sequence 5099, A
Sequence 55999, A
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40.6	40.6	40.6	40.6	40.6	40.6	40.6	40.6	40.6	40.6	40.6	40.6	40.6	40.6	40.6	40.6	40.6	40.6	40.6	40.6	41.7	41.7	41.7	41.7	41.7
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Sequence 2730	Sequence 171,	Sequence 31, 1	•		Sequence 1772,	Sequence 7828,	Sequence 33039,					\sim	Sequence 174,	Sequence 7509,	Sequence 169,		Sequence 4960,	Sequence 1, Appli	Sequence 5831	Sequence 2010,	Sequence 4065	Sequence 5393,	Sequence 5394	Sequence 5395,
•	App	Appl	Appl	App1		Αp	9, A	Appl	Appl	App1	Appl	App	App	γĄ	App	App1	, Ap	ppli	Αp	, Ap	6, A	λp	, Ap	, Ap

ALIGNMENTS

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Sequence 39, Application US/09612314

GENERAL INFORMATION:
APPLICANT: SMITH, Richard, Anthony, Godwin
APPLICANT: DODD, Ian
APPLICANT: DODD, Ian
APPLICANT: MOSSAKOWSKA, Danuta, Ewa, Irena
ITILE OF INVENTION: CONJUGATES OF SOLUBLE PEPTIDIC COMPOUNDS WITH
ITILE OF INVENTION: MEMBRANE-BINDING AGENTS
FILE REFERENCE: 37945-0004
CURRENT APPLICATION NUMBER: US/09/612,314
CURRENT FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 09/214,913
PRIOR FILING DATE: 1999-03-16
PRIOR APPLICATION NUMBER: PCT/EP97/03715
PRIOR APPLICATION NUMBER: GB 96 148 71.3
PRIOR FILING DATE: 1997-07-08
PRIOR APPLICATION NUMBER: GB 96 148 71.3
PRIOR FILING DATE: 1996-07-15
NUMBER OF SEQ ID NOS: 67
SOCTWARE: Patentin Ver. 2.1
SEQ ID NO 39
LENGTH: 70
TYPE: PRT
ORGANISM: Artificial Sequence
                    RESULT 2
US-09-612-314-42
Sequence 42, Application US/09612314
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                  PEATURE:
; OTHER INFORMATION: Description of Artificial US-09-612-314-39
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US-09-612-314-39
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Best Local Similarity
Matches 17; Conserv
APPLICANT: SMITH, Richard, Anthony, Godwin
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                                                                                                                                       100.0%; ilarity 100.0%; Conservative 0
                                                                                                                                                                                                                     0,
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Pred. No.
                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                        Length 70;
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RESULT: 4
US-09-612-314-40
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APPLICANT: DODD, Ian
APPLICANT: MOSSAKOWSKA, Danuta, Ewa, Irena
ITILE OF INVENTION: CONJUGATES OF SOLUBLE PEPTIDIC COMPOUNDS WITH
FILE REFERENCE: 37945-0004
CURRENT APPLICATION NUMBER: US/09/612,314
PRIOR APPLICATION NUMBER: US 09/214,913
PRIOR FILING DATE: 1990-03-16
PRIOR FILING DATE: 1999-03-16
PRIOR FILING DATE: 1997-07-08
PRIOR APPLICATION NUMBER: CT/EP97/03715
PRIOR APPLICATION NUMBER: GB 96 148 71.3
PRIOR FILING DATE: 1997-07-15
PRIOR FILING DATE: 1996-07-15
                                                                                                                                                                                                           ; OTHER INFORMATION: Description of Artificial Sequence: Protein APT631
US-09-612-314-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: MOSSAKOWSKA, Danuta, Ewa, Irena
ITILE OF INVENTION: CONJUGATES OF SOLUBLE PEPTIDIC COMPOUNDS WITH
ITILE OF INVENTION: MEMBRANE-BINDING AGENTS
CURRENT STATEMENT: 37945-0004
CURRENT APPLICATION NUMBER: US/09/612,314
PRIOR APPLICATION NUMBER: US 09/214,913
PRIOR APPLICATION NUMBER: US 09/214,913
PRIOR APPLICATION NUMBER: DS 09/214,913
PRIOR APPLICATION NUMBER: PCT/EP97/03715
PRIOR APPLICATION NUMBER: PCT/EP97/03715
PRIOR APPLICATION NUMBER: GB 96 148 71.3
PRIOR FILING DATE: 1997-07-08
PRIOR FILING DATE: 1996-07-15
SPOID NO 42
LENGTH: 71
TYDER: DEM
                                                                                                                               Query Match
Best Local Similarity 100.
77, Conservative
                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 67
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 37
LENGTH: 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                          TYPE: PRT
                                                                                       42
                                                                                              1 FEHCNFNDVTTRLRENE 17
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                                                                          FEHCNFNDVTTRLRENE 58
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100.0%; Pr
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Pred. No. 3.3e-09
0; Mismatches 0
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Pred. No.
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thes 0;
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В
                           Qy
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В Qy

43 FEHCNFNDVTTRLRENE 59

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CURRENT APPLICATION NUMBER: US/09/612,314
PRIOR APPLICATION NUMBER: US/09/612,314
PRIOR APPLICATION NUMBER: US 09/214,913
PRIOR FILLING DATE: 1999-03-16
PRIOR FILLING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: PCT/EP97/03715
PRIOR APPLICATION NUMBER: GB 96 148 71.3
PRIOR APPLICATION NUMBER: GB 96 148 71.3
NUMBER OF SEQ ID NOS: 67
SOPTWARE: Patentin Ver. 2.1
LENGTH: 83
TYPE: PRT
TOTAL PRIOR TILLING DATE: 1996-07-15
SOPTWARE: PATENTIN VER. 2.1
                                                                                                                                                 ; OTHER INFORMATION: Description of Artificial Sequence: Protein APT635 US-09-612-314-41
                                                                 Matches
                                                                                        Query Match
Best Local
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PRIOR APPLICATION NUMBER: US/09/612,314
PRIOR APPLICATION NUMBER: US 09/214,913
PRIOR FILING DATE: 1999-03-16
PRIOR APPLICATION NUMBER: PCT/EP97/03715
PRIOR APPLICATION NUMBER: PCT/EP97/03715
PRIOR FILING DATE: 1997-07-08
PRIOR APPLICATION NUMBER: GB 96 148 71.3
PRIOR FILING DATE: 1996-07-15
SOFTWARE: PATENTIA NOS: 67
SOFTWARE: PATENTIA VET. 2.1
LENGTH: 82
TYDE: DDT
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US-09-612-314-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 41, Application US/09612314 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: MOSSAKOWSKA, Danuta, Ewa, Irena
TITLE OF INVENTION: CONJUGATES OF SOLUBLE PEPTIDIC COMPOUNDS WITH
FILE REFERENCE: 37945-0004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                     ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: DODD, Ian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: SMITH, Richard, Anthony, Godwin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: DODD, IAN
APPLICANT: MOSSAKOWSKA, Danuta, Ewa, Irena
TITLE OF INVENTION: CONJUGATES OF SOLUBLE PEPTIDIC COMPOUNDS WITH
FILE REFERENCE: 37945-0004
FILE REFERENCE: 37945-0004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 40, Application US/09612314 GENERAL INFORMATION:
1 FEHCNFNDVTTRLRENE 17
                                                               local Similarity les 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 FEHCNFNDVTTRLRENE 17
                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                          100.0%; Score 96; DB 6; I
100.0%; Pred. No. 3.6e-09;
ative 0; Mismatches 0;
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Pred. No. 3.6e-09;
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                                                                             Length 83
                                       Indels
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Best Local Similarity
Matches 17; Conserv
                                           SEQ ID NO 43
LENGTH: 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 43, Application US/09612314 GENERAL INFORMATION:
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APPLICANT: MOSSAKOWSKA, Danuta, Ewa, Irena
TITLE OF INVENTION: CONJUGATES OF SOLUBLE PEPTIDIC COMPOUNDS WITH
TITLE OF INVENTION: MEMBRANE-BINDING AGENTS
FILE REFERENCE: 37945-0004
                                                                                          PRIOR APPLICATION NUMBER: PCT/EP97/03715
PRIOR FILING DATE: 1997-07-08
PRIOR PPLICATION NUMBER: GB 96 148 71.3
PRIOR FILING DATE: 1996-07-15
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                        APPLICANT: MOSSÁKOWSKA, Danuta, Ewa, Irena
TITLE OF INVENTION: CONJUGATES OF SOLUBLE PEPTIDIC COMPOUNDS WITH
TITLE OF INVENTION: MEMBRANE-BINDING AGENTS
FILE REFERENCE: 37945-0004
CURRENT APPLICATION NUMBER: US/09/612,314
CURRENT FILING DATE: 2000-07-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: PCT/EP97/03715
PRIOR FILING DATE: 1997-07-08
PRIOR APPLICATION NUMBER: GB 96 148 71.3
PRIOR FILING DATE: 1996-07-15
NUMBER OF SEQ ID NOS: 67
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: SMITH, Richard, Anthony, Godwin
APPLICANT: DODD, Ian
APPLICANT: MOSSAKOWSKA, Danuta, Ewa, Iren
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CURRENT FILING DATE: 2000-07-07
                                                                                                                                                                                                                                             PRIOR FILING DATE: 1999-03-16
                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 09/214,913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-612-314-45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: UNSURE LOCATION: (71)...(72)
LOCATION: (71)...(72)
OTHER INFORMATION: Residues 1-71 are a first polypeptide chain and OTHER INFORMATION: residues 72-88 are a second polypeptide chain OTHER INFORMATION: linked by a disulphide bond formed between the OTHER INFORMATION: cysteines at positions 71 and 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                         TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: The C-terminal glycine is linked to an OTHER INFORMATION: NH-[Myristoyl] group OTHER INFORMATION: Description of Artificial Sequence: Protein APT2065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: UNSURE LOCATION: (88)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q ID NO 45
LENGTH: 88
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 FEHCNFNDVTTRLRENE 17
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Pred. No. 3.9
0; Mismatches
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APPLICANT: SMITH, Richard, Anthony, Godwin
APPLICANT: DODD, Ian
APPLICANT: MOSSAKOWSKA, Danuta, Ewa, Irena
TITLE OF INVENTION: CONGUGATES OF SOLUBLE PEPTIDIC COMPOUNDS WITH
TITLE OF INVENTION: MEMBRANE-BINDING AGENTS
FILE REFERENCE: 37945-0004
CURRENT APPLICATION NUMBER: US/09/612,314
CURRENT APPLICATION NUMBER: US 09/214,913
PRIOR FILING DATE: 1999-03-16
PRIOR APPLICATION NUMBER: PCT/EP97/03715
PRIOR APPLICATION NUMBER: DCT/EP97/03715
PRIOR APPLICATION NUMBER: DCT/EP97/03715
PRIOR APPLICATION NUMBER: DCT/EP97/03715
PRIOR PILING DATE: 1997-07-08
PRIOR FILING DATE: 1997-07-15
PRIOR FILING DATE: 1997-07-15
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                                            Qy
                                                                                                                                                                                                       ; OTHER INFORMATION: US-09-612-314-44
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Best Local S
Matches 17
                                                                                           Matches
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LENGTH: 100
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                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 67
                                                                                                                                                                                                                        OTHER INFORMATION: The C-terminal glycine is linked to OTHER INFORMATION: NH-[Myristoyl] group OTHER INFORMATION: Description of Artificial Sequence:
                                                                                                                                                                                                                                                                                                                                         NAME/KEY: UNSURE
LOCATION: (83)..(84)
OTHER INFORMATION: Residues 1-83 are a first polypeptide chain and
OTHER INFORMATION: residues 84-100 are a second polypeptide chain
OTHER INFORMATION: linked by a disulphide bond formed between the
OTHER INFORMATION: cysteines at positions 83 and 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (82)..(83)
OTHER INFORMATION: Residues 1-82 are a first polypeptide chain and OTHER INFORMATION: residues 83-99 are a second polypeptide chain OTHER INFORMATION: linked by a disulphide bond formed between the OTHER INFORMATION: cysteines at positions 82 and 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: The C-terminal glycine is linked to an OTHER INFORMATION: NH-[Myristoyl] group OTHER INFORMATION: Description of Artificial Sequence: Protein APT2062
                                                                                                                                                                                                                                                                                              NAME/KEY: UNSURE LOCATION: (100)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
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    43
                                                                                           Local Similarity
les 17; Conser
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les 17; Conser
                                               1 FEHCNFNDVTTRLRENE 17
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FEHCNFNDVTTRLRENE 59
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                                                                                           Conservative
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                                                                                                            100.0%;
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Pred. No.
                                                                                         Score 96; DB 6;
Pred. No. 4.5e-09;
Mismatches 0;
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                                                                                                                                      Length 100
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                                                                                           Indels
                                                                                                                                                                                                                               Protein APT2063
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RESULT

Sequence 20,

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Query Match
Best* Local Similarity 40.08
Watches 6; Conservative
                                                                                                                                ; ORGANISM: DROSOPHILA US-09-614-150-5766
                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: 60/160,191
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR PILING DATE: 1999-11-12
PRIOR PILING DATE: 1999-11-28
PRIOR FILING DATE: 1999-11-27
PRIOR PILING DATE: 1999-11-27
PRIOR PILING DATE: 1999-11-28
PRIOR PILING DATE: 1999-11-28
PRIOR FILING DATE: 1999-12-28
PRIOR FILING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR FILING DATE: 2000-02-24
DEFIOR APPLICATION NUMBER: 60/184,831
PRIOR FILING DATE: 2000-02-24
                                                                                                                                                                                                                SEQ ID NO 5766
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; ORGANISM: Homo sapiens
US-09-673-032-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5766, Application US/09614150
GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
APPLICANT: et al.
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: DEOSOBHILA GENES.
                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 43008
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/191,637 PRIOR FILING DATE: 2000-03-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: CL000728
CURRENT APPLICATION NUMBER: US/09/614,150
CURRENT FILING DATE: 2000-07-11
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Best Local Similarity
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PRIOR FILING DATE: 1999-04-08
PRIOR APPLICATION NUMBER: GB 9807520.3
PRIOR FILING DATE: 1998-04-09
SUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 20
SEQ ID NO 20
                                                                                                                                                                                             LENGTH:
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TITLE OF INVENTION: MODIFIED BIOLOGICAL MATERIAL
FILE REFERENCE: WN/KH/JJ/WCM
CURRENT APPLICATION NUMBER: US/09/673,032
CURRENT FILING DATE: 2000-12-06
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APPLICANT: HINCHLIFFE, STEWART J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: MORGAN, APPLICANT: RUSHMEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 128
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                                                                                                                                                                                             739
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nilarity 100.0%;
Conservative 0
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                                             44.88;
40.08;
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                                         Score 43; DB
Pred. No. 40;
                      Pred. No. 40;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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Pred. No. 5.9e-09;
0; Mismatches 0;
                                                           6;
                                                     Length 739;
                  Indels
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              0;
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          Gaps
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          0,
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SOTTWARE: PatentIn version
SEQ ID NO 15
LENGTH: 236
TYPE: PAT
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(236)
OTHER INFORMATION: 'x' ce
                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/991,630
CURRENT FILING DATE: 2001-11-06
PRIOR APPLICATION NUMBER: 09/905,129
PRIOR FILING DATE: 2001-07-13
PRIOR PRIOR DATE: 2001-07-13
PRIOR PPLICATION NUMBER: 09/802,318
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: 09/729,485
PRIOR FILING DATE: 2000-12-04
NUMBER OF SEQ ID NOS: 28
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NAME/KEY: miso_feature

LOCATION: (1)..(236)

OTHER INFORMATION: 'x' can be any amino acid

US-09-991-630-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 15, Application US/09991630 GENERAL INFORMATION:
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Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn version 3.0 SEQ ID NO 12 LENGTH: 236 TYPE: PRT ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
US-09-991-630-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: GENES ASSOCIATED WITH MECHANICAL STRESS, EXPRESSION PRODUCTS T
TITLE OF INVENTION: AND USES THERBOF
FILE REFERENCE: 540579-2007.3
CURRENT APPLICATION NUMBER: US/09/991,630
PRIOR APPLICATION NUMBER: 09/905,129
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-03-08
PRIOR FILING DATE: 2001-03-08
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-12-04
PRIOR FILING DATE: 2000-12-04
NUMBER: OF SEQ ID NOS: 28
PRIOR FILING DATE: 2000-12-04
NUMBER: OF SEQ ID NOS: 28
PRIOR FILING DATE: 2000-12-04
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GENERAL INFORMATION:
APPLICANT: Einat, et al
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                                                                                                                                                                                       PatentIn version 3.0
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               be any amino acid
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Pred. No. 20;
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; NAME/KEY: misc_feature; LOCATION: (1)..(236); OTHER INFORMATION: 'x' can be any amino acid US-09-905-129-12
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PRIOR APPLICATION NUMBER: 09/802,318
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: 60/207,821
PRIOR FILING DATE: 2000-05-30
PRIOR APPLICATION NUMBER: 60/084,944
PRIOR APPLICATION NUMBER: 60/085,673
PRIOR APPLICATION NUMBER: 60/085,673
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GENERAL INFORMATION:
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Best Local Similarity
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SEQ ID NO 15
LENGTH: 236
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/905,129

CURRENT FILING DATE: 2001-07-13

CURRENT FILING DATE: 2001-07-13
                                                                                                                                                 PRIOR APPLICATION NUMBER: 09/802,318
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: 60/207,821
PRIOR FILING DATE: 2000-05-30
PRIOR APPLICATION NUMBER: 60/084,944
PRIOR FILING DATE: 1998-05-11
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                                                                                                               PRIOR FILING DATE: 1998-05-11
PRIOR APPLICATION NUMBER: 60/085,673
PRIOR FILING DATE: 1998-05-15
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NUMBER OF SEQ ID NOS: 25
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                                                                                            NUMBER OF SEQ ID NOS: 25
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TYPE: PRT
ORGANISM: Mus musculus
ORGANISM: Mus musculus
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Pred. No. 20;
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Pred. No. 20;
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; OTHER INFORMATION: Xaa is any NAME/KEY: misc_feature; LOCATION: 1..220; OTHER INFORMATION: Ceres Seq. US-09-708-427-16838
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Sequence 16838, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
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CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85384
SOFTWARE: Patentin version 3.1
SEQ ID NO 16838
LENGTH: 220
SEQ ID NO 6395
LENGTH: 240
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Best Local
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Best Local Similarity
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                                                                                  APPLICANT: Malvar, Thomas M.
APPLICANT: Slater, Steven C.
APPLICANT: Spiridonov, Sergei
TITLE OF INVENTION: Xenorhabdus sp. Genome
FILE REFERENCE: 38-21(51847)B
CURRENT APPLICATION NUMBER: US/09/897,516
CURRENT FILING DATE: 2001-06-29
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                                       PRIOR APPLICATION NUMBER: US 60/215, 161
PRIOR FILING DATE: 2000-06-30
NUMBER OF THE PRIOR FILING DATE: 2000-06-30
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                                   NUMBER OF SEQ ID NOS: 8409
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ORGANISM: Arabidopsis thaliana
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                                                                                                                                                                                                            Goldman, Barry S.
Hinkle, Gregory J.
Huesing, Joseph E.
Krasomil-Osterfeld, Karina
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Pred. No.
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Pred. No. 20;
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APPLICANT: Neuber, Lynne
APPLICANT: Yu, Guo-Liang
FILE REFERENCE: MBI-0037
CURRENT APPLICATION NUMBER: US/60/336,049
NUMBER OF SEQ ID NOS: 784
SOFTWARE: Patentin version 3.1
LENGTH: 244
TYPE: PRT
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LOCATION: 1.244
COTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1.244
COTHER INFORMATION: Ceres Seq. ID 1831333
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GENERAL INFORMATION:
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ORGANISM: Arabidopsis thaliana
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Best Local
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SEQ ID NO 16837
LENGTH: 244
TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
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TITLE OF INVENTION: SEQUENCE DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE DETERMINED THEREBY
FILE REFERENCE: 2750-1243p
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT TILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
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Best Local Similarity 53...
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                                                                                                                                                   Heard, Jacqueline
Jiang, Cai-Zhong
Keddie, James
Pilgrim, Marsha
Ratcliffe, Oliver
Reuber, Lynne
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53.3%;
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Pred. No.
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38;
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RESULT 21
US-09-708-427-56000
; Sequence 56000, Application US/09708427
; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
                                                                                                                                           Query Match
Best Local Similarity 63.0%,
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: ROSED et al.

APPLICANT: ROSED et al.

FITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PTZ18C1

CURRENT APPLICATION NUMBER: US/10/092,302

CURRENT FILING DATE: 2002-03-07

NUMBER OF SEQ ID NOS: 1040

Prior Application removed - See File Wrapper or Palm

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 711

LENGTH: 262

TYPE: PRT

COCANICAN Homo sarians
                                                                                                                                                                                                                                  ORGANISM: Homo sapiens US-10-092-302-951
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Best Local Similarity
Yorkshes 7; Conserve
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GENERAL INFORMATION:
APPLICANT: ROSen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT218C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens US-10-092-302-711
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Sequence 711, Applic
GENERAL INFORMATION:
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Best Local Similarity 45.20,
Friends 6; Conservative
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CURRENT FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 1040
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                                                                                                                                                                                                                                                                                               Prior Application removed - SOFTWARE: Patentin Ver. 2.0
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TYPE: PRT
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63.6%;
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63.68;
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Pred. No.
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Mismatches
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Pred. No.

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PCT-US02-03987-15325
Sequence 15325, Application PC/TUS0203987
GENERAL INFORMATION:
APPLICANT: Elitra Pharmaceuticals, Inc.
TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits
TITLE OF INVENTION: Proliferation
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Best Local Similarity
6; Conserv
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; LOCATION: 1. 272
; OTHER INFORMATION: Ceres Seq.
US-09-708-427-56000
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CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PatentIn version 3.1
SEQ ID NO 55999
LENGTH: 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 56000
LENGTH: 272
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
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ORGANISM: Zea mays subsp. mays
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OTHER INFORMATION: Xaa is any
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LOCATION: 1..299
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hes 6; Conserv
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46.2%;
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Pred. No.
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Query Match
Best Local Similarity
Thes 7; Conserve
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US-10-032-585-7381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Candida albicans
PCT-US02-03987-15325
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LENGTH: 394
TYPE: PRT
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CURRENT FILING DATE: 2002-02-02
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
NUMBER OF SEO ID NOS: 15811
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15325
LENGTH: 394
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                           Sequence 15325, Application US/10072851 GENERAL INFORMATION:
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APPLICANT: Charles, Boone
APPLICANT: Howard, Bussey
TITLE OF INVENTION: Gene Disruption Methodologies
FILE REFERENCE: 10182-005-999
                                                                   APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/032,585
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 8000-
SOFTWARE: PatentIn version 3.1
                                 APPLICANT:
APPLICANT: Bussey, Howard TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibit TITLE OF INVENTION: Proliferation
                                                                                                                                                                                                       APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                         APPLICANT: Carr, Grant J. APPLICANT: Xu, H. Howard
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                                                 Roemer, Terry
Jiang, Bo
Boone, Charles
                                                                              Trawick, John D. Yamamoto, Robert T. Roemer, Terry
                                                                                                                                                   Zyskind, Judith W.
                                                                                                                                                                     Ohlsen, Kari L.
                                                                                                                                                                                     Haselbeck,
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Zamudio, Carlos
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53.8%;
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Pred. No.
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Pred. No.
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CURRENT APPLICATION NUMBER: US/10/072,851
CURRENT FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 15811
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15325
LENGTH: 394
TYPE: PRT
ORGANISM: Candida albicans
US-10-072-851-15325
Search completed: April 2, 2002, 09:23:05
Job time: 194 sec
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                                                                                                   Db
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Best Local Similarity 53.8%; Pred. No. 65;
Matches 7; Conservative 3; Mismatches 3; Indels
                                                                                   5 NENDVTTRLRENE 17
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349 NENNVSAELKERE 361
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Title:
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Maximum Match 100%
Listing first 50 summaries
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1: /cgn2_6/ptodata/2,
2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
5: /cgn2_6/ptodata/2,
6: /cgn2_6/ptodata/2,
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length: 2000000000
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Copyright (c) 1993 - 2000 Comp
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/cgn2_6/ptodata/2/iaa/6BCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/backfiles1.pep:*
    Gapext 0.5
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US-08-663-566A-15
US-08-023-610-15
US-08-288-065A-15
US-08-362-240A-15
PCT-US95-10.445-15
US-08-277-231A-12
US-08-473-750-1
US-08-473-750-5
US-08-473-750-5
US-08-473-256-5
US-08-473-256-5
US-08-473-26-5
US-08-473-26-5
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US-08-889-841B-10
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US:08-087-007-3

US:08-687-007-3

US:08-486-777-1

US:08-483-433-3

PCT-US:22-05920-3

US:09-591-435-12

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Sequence 12, Appli
Sequence 12, Appli
Patent No. 5521296
Sequence 13, Appli
Sequence 15, Appli
Sequence 15, Appli
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US-08-472-666-1	US-09-257-490-4	US-08-392-806A-4	US-09-257-490-2	US-08-392-806A-2	US-08-889-841B-39	US-08-889-841B-36	US-08-889-841B-46	US-08-494-168-2	US-09-194-613-5	US-08-576-626A-31	US-09-300-909-19	US-09-410-372-9	US-09-410-372-5	US-08-985-335-9	US-08-985-335-5	US-08-576-626A-53	US-09-092-409-56	US-08-680-726A-56	US-08-821-872-2	US-09-433-598-2	US-08-393-985-10	US-09-156-580-2
Sequence 1, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 2, Appli	Sequence 2, Appli	-	Sequence 36, Appl		Sequence 2, Appli	Sequence 5, Appli	Sequence 31, Appl	Sequence 19, Appl			Sequence 9, Appli	~	`	Sequence 56, Appl			Sequence 2, Appli	Sequence 10, Appl	Sequence 2, Appli

ALIGNMENTS

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RESULT 1
US-08-271-562-1
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                                                                                                                                  FILING DATE:

CLASSIFICATION 2435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/729926
FILING DATE: 15-JUL-1991
APPLICATION NUMBER: US 07/365199
FILING DATE: 04-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: PAbst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRF 112C:
TELEPHONE: (444) 815-6508
TELEPHONE: (444) 815-6508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                      TELEFAX: (404) 815-6555 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/271,562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Sims, Peter J.

APPLICANT: Bothwell, Alfred L.M.

TITLE OF INVENTION: Genetic Inhibition of Complement
TITLE OF INVENTION: Mediated Inflammatory Response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1100 Pea
CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.
ZIP: 30309-4530
STRANDEDNESS:
TOPOLOGY: lir
                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30309-4530
                                  amino acids
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    linear
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                     single
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US-08-087-007-3
                                 FRAGMENT TYPE: N-terminal ORIGINAL SOURCE: ORGANISM: Homo sapiens IMMEDIATE SOURCE: CLONE: CD59
                                                                                                                                                                                                                                              ATTORNEY_AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-815-6500
                                                                                                           MOLECULE TYPE: I
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                         TELEFAX: 404-815-6555
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-087-007-3
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                                                                                                                                                                                                                                                                                                                                                             ZIP: 30309-1000
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-BOS/MS-DOS
OPERATION PATENTIN Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/087,007
FILING DATE: 1930701
CLASSIFICATION: 435
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FRAGMENT TYPE: inter....
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: Blood
OPIT. TYPE: Erythrocyte
                                                                                                                                                                 STRANDEDNESS:
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Squinto, TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Kill
STREET: 1100 P.
CITY: Atlanta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.
ZIP: 30309-4530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42 FEHCNFNDVTTRLRENE 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 100.0%; Score 96; DB 1; Local Similarity 100.0%; Pred. No. 4.8e-09; hes 17; Conservative 0; Mismatches of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 FEHCNFNDVTTRLRENE 17
                                                                                                                                                                                 amino acid
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                                                                                                                                                                                        103 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Georgia
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INVENTION: Universal Donor Cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/08087007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1100 Peachtree Street, Suite 2800
                                                                                                                                                        linear
                                                                                                                              NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rollins, Scott
Bell, Leonard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bothwell, Alfred L.M. Elliott, Eileen A. Flavell, Richard A.
                                                                                             N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Madri, Joseph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sims, Peter J
                                                                                                                                         protein
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                                                                                                                                                                   single
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                                            US-08-483-433-3
Sequence 3, Application US/08483433; Patent No. 6100443
GENERAL INFORMATION:
                                                                                                                           RESULT
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Best Local Similarity
Matches 17; Conserve
                                                                                                                                                                                                                                                                                         US-08-696-777-1
                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DC
SOFTWARE: Patentin Release #1.
APPLICATION UNMBER: US/08/696,
ELLING DATE: 13-AUG-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRE
                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (404)-873-8734
TELEFAX: (404)-873-8794
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-696-777-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ъ
            APPLICANT: Sims et al.
TITLE OF INVENTION: UT
NUMBER OF SEQUENCES: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Qy
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNING
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC COMPATIBLE
TOPPOS/MS-DOS
TOPPOS/MS-DOS
TOPPOS/MS-DOS
TOPPOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08696777
Patent No. 5955441
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
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Best Local
                                                                                                                                                      42 FEHCNFNDVTTRLRENE 58
                                                                                                                                                                         1 FEHCNFNDVTTRLRENE 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center, 1201 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Sims, Peter, J.
APPLICANT: Botthwell, Alfred, L. M.
TITLE OF INVENTION: Genetic Inhibition of Complement Mediated
TITLE OF INVENTION: Inflammatory Response
                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
TOPOLOGY: 1i
                                                                                                                                                                                                                                                                                                                                                            LENGTH:
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                                                                                                                                                                                                                                                                                                                                         amino acid
                                                                                                                                                                                                                                                                                                                                                    103 amino acids
                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                   peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                  Universal Donor Cells
                                                                                                                                                                                                                 100.0%; Score 96; DB 2; 100.0%; Pred. No. 4.8e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Release #1.0, Version #1.25
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ative 0;
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                                                                                                                                                                                                                            Length 103;
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Patrea L. Pabst

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                                                                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                      Sequence 3, Application:
                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGI,
MOLECULE TYPE: pro-
MYPOTHETICAL: NO
"YMT-SENSE: NO
"YDE: NO-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY_AGENT INFORMATION:
NAME: PABST, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404_873-8794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 404-873-9794
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 103 amino acids
                                                                                                                        APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRAGMENT TYPE: N-termina ORIGINAL SOURCE: ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/906,
FILING DATE: June 29, 1992
                                              APPLICANT: Squinto, Stephen TITLE OF INVENTION: Universal Donor Cells NUMBER OF SEQUENCES: 4
                                 CORRESPONDENCE ADDRESS:
                                                                                            APPLICANT:
                                                                                                           APPLICANT:
                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 2800 One Atlantic Center STREET: 1201 West Peachtree Street CITY: Atlanta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: Ju CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Georgia COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                    42 FEHCNFNDVTTRLRENE 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                     1 FEHCNFNDVTTRLRENE 17
                                                                                                                                                                                                                                                                                                                                                                ch 100.0%; l Similarity 100.0%; 17; Conservative 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30309-3450
                                                                                                                                                                                                                       Application PC/TUS9205920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CD59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ະຣຣ: single
linear
                                                                                                                                       Bothwell, Alfred L. Elliott, Eileen A. Flavell, Richard A.
                                                                                           Bell, Leonard
                                                                                                         Rollins, Scott
                                                                                                                        Madri, Joseph
                                                                                                                                                                                       Sims, Peter J.
Kilpatrick & Cody
)O Peachtree Street, Suite 2800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                July 1,
                                                                                                                                                                       Alfred L.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08/087,007
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                  4.8e-09;
thes 0;
                                                                                                                                                                                                                                                                                                                                                                                                 DB 3;
                                                                                                                                                                                                                                                                                                                                                                                               Length 103;
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                                                                   CURRENT APPLICATION NUMBER: US/09/591,435
CURRENT FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 09/591,435
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 09/240,915
PRIOR FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: 60/073,263
PRIOR FILING DATE: 1998-01-30
PRIOR FILING DATE: 1998-09-02
PRIOR FILING DATE: 1998-09-02
NUMBER OF SEO ID NOS: 13
                                                                                                                                                                                                                                                                                                                                                                                       US-09-591-435-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCT-US92-05920-3
                                                                                                                                                                                                                                                                                                                                                  Described No. 6280953
                                           SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                      TELEFAX: 404-815-6555
                LENGTH: 105
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: I
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IMMEDIATE SOURCE:
CLONE: CD59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRAGMENT TYPE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-815-6500
TELEFAX: 404-815-6555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: PABST, PATTGA L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 103 amino acids TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 19920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     42 FEHCNFNDVTTRLRENE 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 FEHCNFNDVTTRLRENE 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Linear
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SYSTEM: PC-DOS/MS-DOS
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Pred. No. 4.8e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 103;
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US-09-591-435-12

Query Match Best Local Similarity Matches 17; Conserv

Conservative

100.0%; Score 96; DB 4; L 100.0%; Pred. No. 4.9e-09; A. Mismatches 0;

Length 105; Indels

0;

Gaps

0;

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RESULT ;

$179198-1
;Patent No. 5179198
;Paten
Sequence 13, Application US/09591435
PATENT NO. 6280953
GENERAL INFORMATION:
APPLICANT: MESSIER, WALTER
APPLICANT: SIRELA, JAMES M
CTITLE OF INVENTION: METHODS TO IDENTIFY POLYNUCLEOTIDE AND POLYPEPTIDE
TITLE OF INVENTION: SOUTHOUS WHICH MAY BE ASSOCIATED WITH PHYSIOLOGICAL
TITLE OF INVENTION: AND MEDICAL CONDITIONS
                                                                                                                                                                                                                                                                                                                                       RESULT 9
US-09-591-435-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 5521296

APPLICANT: OKADA, HIDECHIKA; OKADA, NORIKO; NAGAMI, YOICHI;
TAKAHASHI, KAZUHIRC; TAKIZAWA, HISAO; KONDO, JUN

TITLE OF INVENTION: GLYCOPROTEIN AND GENE CODING THEREFOR SEQUENCES: 12
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/739,211
FILING DATE: 01-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 01-JUL-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5521296-1
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5521296-1
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 FEHCNFNDVTTRLRENE 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 100.0%; tocal Similarity 100.0%; tes 17; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 FEHCNFNDVTTRLRENE 17
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es 17; Conserv
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Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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Pred. No. 6.1e-09;
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; MOLECULE TYPE: US-08-663-566A-15
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MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-POS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/663,566A
FILING DATE: June 13, 1996
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION INFORMATION:
FELEPHONE: (212)278-0400
TELEPHONE: (212)278-0400
 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: GENO. 200. 2
CURRENT APPLICATION NUMBER: US/09/591,435
CURRENT FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 09/591,435
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 09/2940,915
PRIOR FILING DATE: 1999-01-29
PRIOR FILING DATE: 1999-01-30
PRIOR FILING DATE: 1998-01-30
PRIOR FILING DATE: 1998-09-02
PRIOR FILING DATE: 1998-09-02
SOPTWARE: PATENTIN VET. 2.0
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; ORGANISM: Pan troglodytes
US-09-591-435-13
                                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 1162 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match

Best Local Similarity 87.5

Matches 14; Conservative
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                                                                                                                                                                    TELLEFAX: (22523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Cochran, Mark D
APPLICANT: Macdonald, Richard D
TITLE OF INVENTION: Recombinant Herpesvirus of Turkeys
NUMBER OF SEQUENCES: 56
NUMBER OF SEQUENCES: 56
                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1185 Aver
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: John P. White
STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44 EHCNFKDLTTRLRENE 59
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                                                                                                  amino acid
)GY: linear
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5853733
                                                                                                                            1162 amino acids
42.7%;
75.0%;
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87.5%;
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Pred. No. 1.8e-06;
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Score Pred.

41; No.

2

Length 1162;

Matches

Conservative

Mismatches

Indels

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US-08-288-065A-15
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                                                                                                                                                                                                      Sequence 15, Application US/08288065A Patent No. 5961982
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                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 15, Application US/08023610 Patent No. 5928648
                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 422523
NFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: White Esq, John P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)977-9550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 1162 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: RECOMDITION: TITLE OF INVENTION: and Uses Thereof
                                                                                                                                          APPLICANT: Cochran, Mark D
APPLICANT: Macdonald, Richard D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Cochran Ph.D, Mark D
APPLICANT: Macdonald Ph.D., Richard D
TITLE OF INVENTION: Recombinant Herpesvirus of Turkeys
                                                                                                                 TITLE OF INVENTION:
                                                                               CORRESPONDENCE ADDRESS
                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                         101 HCNFSDTT 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
            CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                              STREET:
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COUNTRY:
                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                           3 HCNFNDVT 10
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                                                1185 Avenue of the Americas
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                                                                  John P. White
                                                                                                                 Recombinant Herpesvirus of Turkeys S-HVT-050 and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                               42.7%;
75.0%;
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                                                                                                                                                                                                                                                                                                                                                                                               Score 41; DE Pred. No. 97;
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US-08-362-240A-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 422523
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                        TELEX: 422523
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,240A
FILING DATE: Dec-22-94
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,
                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)278-0400
TELEFAX: (212)391-0526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Cochran, Mark I APPLICANT: Junker, David APPLICANT: Wild, Martha A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: li
MOLECULE TYPE:
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NAME: White, John P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                      SEQUENCE CHARACTERISTICS LENGTH: 1162 amino ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
TOPOLOGY: 1
MOLECULE TYPE:
                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101 HCNFSDTT 108
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STATE: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US, FILING DATE: Aug-09-94 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TLE OF INVENTION: Recombinant Herpesvirus and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX:
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                                                                      amino acid
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                                                                                                         1162 amino acids
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75.0%;
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    Mismatches

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Pred. No.
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RESULT 15
US-08-277-231A-2
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               APPLICANT: Brinton, Charles C.

TITLE OF INVENTION: Sequence and Analysis of LKP Pilin

TITLE OF INVENTION: Structural Genes and The LKP Pili Operon of No. 5643725typabl

NUMBER OF ENQUENCES: 14
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TELEFAX: 4252.,
TELEX: 4252.,
TELEX: 4252.,
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 1162 amino acids
myPE: amino acid
myPE: amino acid
                                                                                                                          Sequence 2, Application US/08277231A
Patent No. 5643725
                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: PCT-US95-10245-15
                                                                                  GENERAL INFORMATION:
APPLICANT: Green, Bruce A.
APPLICANT: Brinton, Charle
                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                          Query Match
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Sequence 15, Application PC/TUS9510245
GENERAL INFORMATION:
APPLICANT: SYNTRO CORPORATION
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CORRESPONDENCE ADDRESS:
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NAME: White John P
REGISTRATION NUMBER: 28,678
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)278-0400
TELEFAX: (212)391-0526
                                                                                                                                                                                                                  101 HCNFSDTT 108
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Best Local (
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APPLICATION NUMBER: PCT/US95/10245
FILING DATE: 09-AUG-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                 3 HCNFNDVT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS-MS-DOS
SOFTWARE: Patentin Release #1.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: John P. WHILE
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101 HCNFSDTT 108
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75.08;
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75.0%;
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                                                                                                                                                                                                                                                             Score 41; DB 5; Pred. No. 97; 1; Mismatches
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Pred. No.
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                                                                                                                                                                                                                                                                                        Length 1162;
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/277,231A
FILING DATE: 19-JUL-1994
CLASSIFICATION: 435
APPLICATION: 435
APPLICATION: 435
                                                                                                                                                                                                                                                                             PATENTIAN: Sequence and Analysis of LKP Pilin PATENTIAN: Sequence and Analysis of LKP Pilin PITTLE OF INVENTION: Structural Genes and The LKP Pili C NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
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APPLICANT: Green, Bruce A.
APPLICANT: Brinton, Charles C.
              ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Alice O.
REGISTRATION NUMBER: 32,542
REFERENCE/DOCKET NUMBER: ACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local :
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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TELEFAX: (617) 861-95
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                        COUNTRY: UZIP: 02173
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LENGTH: 217 amino acids
                                                                                                                                                                                                                                                                          STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
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REFERENCE/DOCKET NUMBER: ACC
TELECOMMUNICATION INFORMATION.
TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/OF FILLING DATE: 19-JUL-1994 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: CAITOLI, Alice O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 FEHCNFNDVTTRLRENE 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: UZIP: 02173
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CITY: Lexington
STATE: Massachus
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                                                                                                                                                                                                                                                               Massachusetts
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SYSTEM: PC-DOS/MS-DOS
Patentin Release #1.0, Version #1.30
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Haemophilus Influenzae
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              ACC94-02
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Pred. No.
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Query Match
Best Local Similarity
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US-08-473-750-1
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INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 217 amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Green, Bruce A.
APPLICANT: Brinton, Jr., Charles C.
TITLE OF INVENTION: Sequence and Analysis of LKP Pilin Patent No. 5834187
Patent No. 5834187 5786143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No. 5834187
Patent No. 5834187 5786143
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Best Local :
                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/473,750
FILING DATE: 07-JUN-195
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/277,321
FILING DATE: 19-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Alice 0.
REGISTRATION UNMBER: 33,542
REFERENCE/DOCKET NUMBER: ACC94-02B
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 1:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Structural Gene and the LKP Pili Operon of No. 5834187 578614: TITLE OF INVENTION: Haemophilus Influenzae NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
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Local Similarity 47.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 217 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                       LENGTH: 217 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: Two Mil. CITY: Lexington
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                                                                                                                                          TOPOLOGY:
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617-861-9540
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                Conservative
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                                                                                                                                            linear
                                                                                                                        peptide
                                                                                                                                                     single
                                41.78;
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                Score 40; DB 2;
Pred. No. 22;
2; Mismatches
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Pred. No.
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                Indels
                0;
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                Gaps
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US-08-477-326-1
Sequence 1, Application US/08477326
Patent No. 5968769
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Best Local Similarity
"hes 8; Conserve
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,750
EILING DATE: 07-UNU-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/277,321
FILING DATE: 19-UNL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Alice O.
REGISTRATION NUMBER: 33,542
REFERENCE/DOCKET NUMBER: ACC94-02B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No. 5834187 5786143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Green, Bruce A.
APPLICANT: Brinton, Jr., Charles C.
APPLICANT: Brinton, Sequence and Analysis of LKP Pilin
GENERAL INFORMATION:
APPLICANT: Green, Bruce A.
APPLICANT: Brinton, Jr., Charles C.
APPLICANT: Brinton, Jr., Charles C.
TITLE OF INVENTION: Sequence and Analysis of LKP Pilin
                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 217 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Structural G
TITLE OF INVENTION: Haemophilus
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Sm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                             156 FTHSNTNDVATQQTVNK 172
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TYPE: a
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CITY: Lexington
STATE: Massachus
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                                                                                                                                                                                                                                                                                          41.78;
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Pred. No. 22;
                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                              Length 217;
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TITLE OF INVENTION:

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US-08-477-326-5
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Best Local Similarity
""" hes 8; Conserve
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MOLECULE TYPE:
US-08-477-326-1
                                                                                                                                                                                                                                                               Patent No.
                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/08477326 Patent No. 5968769
                        COMPUTER READABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                               TITLE OF INVENTION: Structural Gene and the LKP Pili
NUMBER OF SEQUENCES; 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
                                                                                                                                                                                                                                          APPLICANT: Green, Bruce A.
APPLICANT: Brinton, Jr., Charles C.
TITLE OF INVENTION: Sequence and Analysis of LKP Pilin
tent No. 5968769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
APPLICATION NUMBER: US/08/477,326
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                            156 FTHSNTNDVATQQTVNK 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/2:
FILING DATE: July 19, 199
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                      1 FEHCNFNDVTTRLRENE 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Carroll, Alice REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                       02173
                                                                                                                                           Massachusetts
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Pred. No. 22;
2; Mismatches
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                                 Version #1.30
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Best Local Similarity
""" 8; Conserve
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; OTHER INFORMATION: SIVCPZ
US-09-257-490-15
 Sequence 4, Application US/08392828C
Patent No. 5795962
GENERAL INFORMATION:
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No. 6248328
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APPLICANT:
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Best Local (
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В

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APPLICANT: Dietrich, Ursula
APPLICANT: Von Briesen, Hagen
APPLICANT: Von Briesen, Hagen
APPLICANT: Von Briesen, Hagen
APPLICANT: Wind Briesen, Hagen
APPLICANT: Rubsamen-Waigmann, Helga
TITLE OF INVENTION: diagnostics, a vaccine against HIV-1 virus infections
TITLE OF INVENTION: of this subtype and method of producing same, use of
TITLE OF INVENTION: the HIV-1 virus isolates
TITLE FERENCE: 10496/P585120S1
CURRENT APPLICATION NUMBER: US/09/257,490A
NUMBER OF SEO ID NOS: 15
SOFTWARE: patentin Ver. 2.1
                                                                                                                                                                     ORGANISM: Simian immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
45 KNCSFN-VTTELRDKK 59
                           2 EHCNFNDVTTRLRENE 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              156 FTHSNTNDVATQQTVNK 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EKVOL...
LENGTH: 21, ...
TYPE: amino acid
Tinear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/27
FILING DATE: July 19, 19;
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 47.1 hes 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 FEHCNFNDVTTRLRENE 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 617-861-9540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Carroll, Alice O.
REGISTRATION NUMBER: 33,542
REFERENCE/DOCKET NUMBER: AC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/477,326 FILING DATE: 07-JUN-1995 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _Application US/09257490A
                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         217 amino acids
                                                                        41.18; 50.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41.7%;
47.1%;
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                                                                    Score 39.5;
Pred. No. 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2
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Pred. No.
                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACC94-02A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                  DB
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                                                                           Length 602;
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                                                 Indels
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                                          Gaps
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                                         1;
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APPLICANT:
APPLICANT:

MUTA, TATSUSHI . SEKI, NORIAKI

TOSHIO

TITLE OF INVENTION: NOVEL POLYPEPTIDE AND DNA ENCODING TITLE OF INVENTION: THEREOF

NUMBER OF SEQUENCES:

39

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Best Local Similarity
""" hes 6; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-330-945-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-392-828C-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER KEADABLE FORM:

MEDIUM TYRE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/392,828C
FILING DATE: 28-FEB-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, PAULA A
REGISTRATION NUMBER: 32,503
REFERENCE/DOCKET NUMBER: FJN-033
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7100
TELEPHONE: (617) 248-7100
TELEPAX: (617) 248-7100
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/09330945 Patent No. 6077946 GENERAL INFORMATION:
                                                                                                                                                                                                                                           APPLICANT: MUTA, TATSUSHI
APPLICANT: MUTA, TATSUSHI
APPLICANT: SEKI, NORIAKI
APPLICANT: ODA, TOSHIO
TITLE OF INVENTION: DNA ENCODING HORSESHOE CRAB
TITLE OF INVENTION: AMEBOCYTE LYSATE FACTOR G SUBUNIT
TITLE OF SEQUENCES: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
ADDRESSEE: THIBEAULT
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 278 amino TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 53 ST
CITY: BOSTON
                                                                                                                                             STATE: MA
                                                                                                                                                                                      STREET:
                                                                                                      COUNTRY: U
                                                                                                                                                                     CITY: BOSTON
                                                                                                                                                                                                         ADDRESSEE: PATENT ADMINIST ADDRESSEE: THIBEAULT, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 KHCGFRPVITRI 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 EHCNFNDVTTRL 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39.6%; ilarity 50.0%; Conservative
                                                                                                                            USA
                                                                                                                                                                                                                               PATENT ADMINISTRATOR, TESTA, HURWITZ &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 38;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 278, 63;
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PATENT NO. 5840695

PATENT NO. 5840695

PARENT INFORMATION:
APPLICANT: FRANK, GLENN R.
APPLICANT: HUNTER, SHIRLEY WU
APPLICANT: WALLENFELS, LYNDA
TITLE OF INVENTION: NOVEL ECTOPARASITE SALIVA PROTEINS
TITLE OF INVENTION: AND APPARATUS TO COLLECT SUCH PROTEINS
TITLE OF SEQUENCES: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 24
US-08-630-822A-70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein US-09-330-945-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 39.6%;
Best Local Similarity 50.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 70, Application US/08630822A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEPAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                             APPLICATION NUMBER: US/08/630
FILING DATE: 11-APR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CONNELL, GARY J.
REGISTRATION NUMBER: 2618
REFERENCE/DOCKET NUMBER: 2618
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
                                                                                                            TELEFAX: (303) 863-0223 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
CONPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDMUND R
REGISTRATION NUMBER: 27,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/330,945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                 MOLECULE TYPE:
                                                                                         SEQUENCE CHARACTERISTICS:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: C
                               TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Denver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 278 amino acids TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 80203
                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 KHCGFRPVITRI 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 EHCNFNDVTTRL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Colorado
                                                                      586 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                     U.S.A.
                 protein
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                                                                                                              70:
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                                                                                                                                                                                        2618-17-C3
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Pred. No. 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 278;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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0

Search completed: April 2, 2002, 09:20:32 Job time: 41 sec

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GENERAL INFORMATION:
APPLICANT: FRANK, GLENN R.
APPLICANT: WALLENEELS, LIVA WU
APPLICANT: WALLENEELS, LIVA
TITLE OF INVENTION: NOVEL ECT
TITLE OF INVENTION: NOVEL ECT
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS;
ADDRESSEE: Sheridan Ross P.C.
CITY: Denver
STREET: 1700 Lincoln Street, Suite 3500
STREET: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM C compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION NUMBER: US/09/005,069
FILING DATE:
CLASSIFICATION NUMBER: US/09/005,069
FILING DATE: 11-APR-196
APPLICATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 32,020
TELECOMMONICATION INFORMATION:
REFERENCE (303) 863-0233
SEQUENCE CHARACTERISTICS:
LENGTH: 586 amino acidd
TOPOLOGY: linear
MOLECULE TYPE: protein
, 8
                                                                                                                                          MOLECULE TYPE: Protein
FEATURE:
NAME/KEY: Xaa = any amino acid
US-09-005-069-70
                                                                         Query Match
Best Local S
Matches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 25
US-09-005-069-70
; Sequence 70, Application US/09005069
; Patent No. 5932470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; NAME/KEY:
; LOCATION:
US-08-630-822A-70
           578 EHCQYPDIT 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 38.5
Best Local Similarity 55.6
Matches 5; Conservative
                                                               hes 5; Conservative
                               2 EHCNFNDVT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                578 EHCQYPDIT 586
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379
                                                  38.5%; Score 37; DB 2; Length 586
55.6%; Pred. No. 2.1e+02;
tive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 37; DB 2; Length 586
Pred. No. 2.1e+02;
2; Mismatches 2; Indels
                                                                                 Length 586;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 586;
                                                  0;
                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                              0;
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Qγ



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Title:
Perfect score:
Sequence:
                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                              Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OM protein - protein search, using sw model
                                                                         Database :
                                                                                                                                                                                                                                                                                                                                 Scoring table:
PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
                                                                                                                                                                                                                                                                                                                                                                                                                                       January 6, 2002, 09:01:52; Search time 37.51 Seconds (without alignments) 54.831 Million cell updates/sec
                                                                                                                                                                                                                                                                          219241 seqs, 76174552 residues
                                                                                                                                                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                   US-09-020-393B-18
145
1 KCLGYHLDVSLAFSEISVGAEFNKDDC 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                            219241
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

44	44	44	44	44	44	44	22 44 30.	44.5	45	45	45	45	45	5.5	45.5	46	46	46	46		46	7 46 31.	46	5 46.5 32.	49		2 52 35.	1 142 97.	No. Score Match	Result Query	dip.
	659	659	560	3 535 2	535	261		884	1189		732	440								7 357 2				1002	524	135	3227	9 559 1	h Length DB	Ÿ	
A46013	B81082	A81862	\$42158	F81094	F81847	A86763	T26909	T18649	T30319	T49010	T18567	C84265	T44333	D81055	C81822	T21712	T25933	JX0368	JQ2174 ·	S27909	C70421	E84826	T30493	T19226	A29677	PN0494	T37964	С9НО	ID		
coagulation factor	transketolase NMB1	transketolase (EC	KRE11 protein - ye	pyruvate dehydroge		cobyric acid synth		hypothetical prote	\mathbf{H}		4	-	hypothetical prote	æ			hypothetical prote	inter-alpha-trypsi		hypothetical prote	⋍				complement C9 prec	NAD+ ADP-ribosyltr	probable ubiquitin	complement C9 prec	Description		

44 5	442 43	4 0	37 38	35 5	33 4	32 32	30
43 43	4 4 4 3 3 3	43.5 43	43.5	43.5	44.5	44	44
29.7 29.7	29.7 29.7 29.7	30.0 29.7	30.0	30.0	30.3	30.3	30.3
311 323	257 305 309	2550 201	739 884	247 341	971 117	679 944	678
N N	N N N	NN	N N	20	NN	– 2	2
S52498 T26536	C64442 F64481 T09564	B53435 A47096	F86337 E86244	T52511 S64618	E96794 H75165	S54299 S48821	A71287
GPM2 protein - yea hypothetical prote	hypothetical prote hypothetical prote glutaminyl-peptide	vesicular transpor response regulator	hypothetical prote unknown protein, 4	related to lysopho hypothetical prote	hypothetical prote hypothetical prote	transketolase (EC	probable cytoplasm

ALIGNMENTS

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A;Description: in association with complement C5b-8 complex polymerizes to form a transm C;Superfamily: complement Dathway
C;Superfamily: complement C9; EGF homology; LDL receptor ligand-binding repeat homology;
F;1-21/Domain: complement pathway; cytolysis; glycoprotein; inflammation; membrane attack CF;22-265,266-559/Product: complement C9; status predicted <SIG>F;22-265/Domain: complement C9; status predicted <C9A>F;41-95/Domain: complement C9 #status predicted <C9A>F;101-134/Domain: thrombospondin type 1 repeat homology <THR>F;265-559/Domain: complement C9b #status predicted <C9A>F;101-34/Domain: LDL receptor ligand-binding repeat homology <LDL>F;101-34/Domain: complement C9b #status predicted <C9B>F;43-7839/Domain: complement C9b #status predicted <C9B>F;43-7839/Domain: EGF homology <EGF>F;43-783-788-94.142-181,254-255,380-405,510-526,513-528,530-539/Disulfide bonds: #stf:51/Modified site: 2'-mannosyl-tryptophan (Trp) #status experimental F;265-266/Cleavage site: His-Gly (thrombin) #status predicted
F;277,415/Binding site: carbohydrate (Asn) (covalent) #status predicted
                           B
                                                              Qγ
                                                                                                                                                                                                                                    A;Residues: 1-3227 <DEV>
A;Residues: 1-3227 <DEV>
A;Cross-references: EMBL:Z99531; PIDN:CAB16714.1; GSPDB:GN00066; SPDB:SPAC19D5.04
A:Experimental source: strain 972h-; cosmid c19D5
                                                                                                                                                                                                                          A; Map position:
                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                 R;Devlin, K.; Churcher, C.M.; Wood, V.; Barrell, B.G.; submitted to the EMBL Data Library, September 1997 A;Reference number: Z21757 A;Accession: T37964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable ubiquitin ligase - fission C:Species: Schizosaccharomyces pombe C:Date: 03-Dec-1999 #sommon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Accession: T37964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q
                                                                                                             Matches
                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GDB:119738; OMIM:120940
A;Map position: 5p13-5p13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Biol. Chem. 274, 32786-32794, 1999
A;Title: The four terminal components of the complement system are C-mannosylated
A;Reference number: A59362; MUID:20020247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 27-559 <WIT>
A; Cross-references: GB:Y08545; NID:g1834472; PIDN:CAA69849.1; PID:g2258128
A; Experimental source: macronuclear; tissue type blood; cell type lymphocyte
A; Experimental source: M: Hess, D.; Furmanek, A.; Miroshnichenko, O.

Biol. Chem. 274, 32786-32794, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local (
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A;Status: preliminary; not compared with conceptual translation
1339 CILYLLEVLLADSKKPDEFEFNSEDC 1364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genetics:
                                                                                                                                 Local
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                                            CLGYHLDVSLAFSEISVGAEFNKDDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RCLGYHLDVSLAFSEISVGAEFNKDDC 405
                                                                                                             l Similarity
12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                plasma; 10 to 16 chain multimer in transmembrane
                                                                                                                       35.98;
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96.3%;
                                                                                                               Score 52;
Pred. No.
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Pred. No. 2.6e-14;
1; Mismatches 0;
                                                                                       Mismatches
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                                                                                                                                 DB 2;
                                                                                       10;
                                                                                                                            Length 3227;
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                                                                                  Indels
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A; Molecule type: DNA
A; Residues: 1-1002 <
                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                              A;Reference number:
A;Accession: T19226
                                                                                                        submitted to the EMBL Data Library, A;Reference number: Z19093
                                                                                                                                                 hypothetical protein C13B4.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T19226
                                                                                                                                                                                                                                                        RESULT
T19226
                                                                                                                                                                                                                                                                                                                                 Ъ
                                                                                                                                                                                                                                                                                                                                                                  Qγ
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C;Superfamily: complement C9; EGF homology; LDL receptor ligand-binding repeat homology; C;Keywords: complement alternate pathway; complement pathway; cytolysis; glycoprotein F;19-73/Domain: thrombospondin type 1 repeat homology <THR>
F;79-112/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F;489-518/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBO J. 6, 1951-1957, 1987
A;Title: Topological mapping of complement component C9 by A;Reference number: A29677; MUID:88004404
A;Molecula terri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-524 <STA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement C9 precursor - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
A29677
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A: Residues: 1-135 <OZA>
C; Comment: This zinc-finger protein plays a role in
C; Superfamily: NAD+ ADP-ribosyltransferase
C; Keywords: DNA binding; glycosyltransferase; hexosy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: PN0494
R;Dzawa, Y.; Uchida, K.; Uchida, M.; Ami, Y.; Kushida, S.; Okada, N.; Miwa, M. Biochem. Biophys. Res. Commun. 193, 119-125, 1993
A;Title: Isolation of cDNAs encoding the catalytic domain of poly(ADP-ribose)polymera;Reference number: PN0494; MUID:93277538
A;Accession: PN0494
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PN0494
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Best Local
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                                                                                                                                                                                                                                                                                                             354 CLGFNMDLRIPLQDDLKDASVTASVNADGC 383
                                                                                                                                                                                                                                                                                                                                                2 CLGYHLDVSLA----FSEISVGAEFNKDDC 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 LDIEVAYSLLKGGAEDNKKD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10;
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                                             <WIL>
EMBL:281468; PIDN:CAB03875.2; GSPDB:GN00020; CESP:C13B4.1
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                                                                                                                                                                                                                                                                                                                                                                                                           33.8%;
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                                                                                                                                                                                                                                                                                                                                                                                            6;
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Pred. No. 11;
                                                                                                                          November 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4;
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1; Mismatches
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Pred. No. 2
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2.5;
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: E84826
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, C.
Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source: C; Genetics:
                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-254 <S
A; Cross-references: 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 1-203 <KUZ>
A;Cross-references: EMBL:AF081810; NID:g3822234; PIDN:AAC70329.1;
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                               Q
                                                                                                                                                                                                                                              A; Reference number: A84420; A; Accession: E84826
                                                                                                                                                                                                                                                              A; Title: Sequence and analysis of chromosome 2
A; Reference number: A84420; MUID:20083487
                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein At2g40200 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
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Best Local S
Matches 14
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Best Loc
Matches
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      36
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                                                                               Local
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nes 10; Conserv
                                                                                                                                          At2g40200
osition: 2
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                                   SLAFSEISVGAEFNKDDC
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      NLGFSSSSFGGNFPADDC
                                                                                                                                                                                                   1-254 <STO>
                                                               Similarity 50.(
9; Conservative
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                                                                                                                                                                                     GB:AE002093;
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                                                                            31.7%;
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43.8%;
      53
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4; Mismatches
                                                                                                                                                                                   NID:g6598939;
                                                                            Score 46;
Pred. No.
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Pred. No. 53;
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                                                                 Mismatches
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                                                                                                                                                                                   PIDN: AAF18734.1;
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                                                                                            Length
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                                                                                                                                                                                                                                                                             plant Arabidopsis thaliana.
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                                                                                                                                                                                   GSPDB:GN00139
                                                              0;
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A; Molecule type: mRNA
A; Residues: 1-357 <SUM>
C; Superfamily: garlic virus
                                            R:Sumi, S.; Tsuneyoshi, T.; Furutani, H.
J. Gen. Virol. 74, 1879-1885, 1993
A;Title: Novel rod-shaped viruses isolated
A;Reference number: JQ2171; MUID:93389442
A;Accession: JQ2174
                                                                                                                                    hypothetical 39.2K protein (clone GV-A) - garlic vC;Species: garlic virus BC;Date: 30-Sep-1993 #sequence_revision 20-Aug-1994
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JQ2174
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C70421
                                                                                                                       C; Accession:
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Best Local S
Matches 10
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Best Local
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                                                                                                                         JQ2174
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B

conserved

hypothetical 39.2K protein

from

garlic,

Allium

sativum,

possessing

garlic virus

#text_change 07-May-1999

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A;Cross-references: EMBL:D11157
C;Superfamily: garlic virus B co
                                                                                                                                                                                                                                                                                                                                 hypothetical protein III - garlic virus C;Species: garlic virus A C;Date: 06-Jan-1995 #sequence_revision C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. A; Reference number: A70300; MUID:98196666 A; Accession: C70421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: C70421
R;Deckert, G.; Warren, P.V.; Gaasterland,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                conserved hypothetical protein aq_1392 -
                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-357 <SUM>
                                                                                                                                                                                                                               A; Status: preliminary
                                                                                                                                                                                                                                                                                     submitted to the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: aq_1392 C; Superfamily: Methanobacterium thermoautotrophicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:AE000738; NID:g2983801; A;Experimental source: strain VF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-292 <AQF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary; nucleic acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  261 LKYELDFRLAFSAITLG
39 RTVGAHVDSSIAFNRINLQTIYN 61
                                 KCLGYHLDVSLAFSEISVGAEFN 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LGYHLDVSLAFSEISVG 19
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                                                                  Similarity 34.8
8; Conservative
                                                                                                                                                                                                                                                                                                                        S27909
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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S27908
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                                                                                   31.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31.7%;
                                                                                                                                                                                                                                                                                   Library,
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                                                                                                                                                          conserved hypothetical 39.2K protein
                                                                                 Score 46;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 46;
Pred. No.
                                                                                                                                                                                                                                                                                   July 1992
                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aquifex aeolicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T.; Young, W.G.; Lenox,
                                                                                   DB
21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB
17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         not shown;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              conserved hypothetical
                                                                                                      Length 357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 292;
                                                                    Indels
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                                                                  Gaps
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hypothetical protein W02C12.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #te: C;Accession: T25933 St. Wohldmann, P. Submitted to the EMBL Data Library, December 1996 A;Description: The sequence of C. elegans cosmid W02C1
A;Description: The sequence of A;Reference number: Z20112
                                                                                                                                                                                                                                                               RESULT
T25933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Albescription: highly sensitive to plasma kallikrein (Superfamily: inter-alpha-trypsin inhibitor complex component II (Superfamily: inter-alpha-trypsin inhibitor complex component II (Superfamily: inter-alpha-trypsin inhibitor complex component II (Superfamily: sequence inhibitor (Superfamily: sequence inter-alpha trypsin inhibitor heavy chain-related protein #status predicted (Superfamily: Superfamily: S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: protein
A;Residues: 29-45;171-184;211-239;274-281;301-315;429-443;488-502;690-695;697-700;703-72
A;Experimental source: liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A:Molecule type: mRNA
A:Residues: 1-84,'1',86-113,'S',115-930 <NIS>
A:Cross-references: EMBL:D38535; NID:g624879; PIDN:BAA07536.1; PID:g1402590
A:Accession: S78548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEBS Lett. 357, 207-211, 1995
A;Title: cDNA and deduced amino acid sequence of human PK-120, a plasma kallikrein-sensi
A;Reference number: S68457; MUID:95104473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: protein
A;Residues: 29-44;48-55;61-75;99-111;140-151;163-169;211-224;246-267;274-281;296-329;39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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A; Residues: 1-930 <SAG1>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Date: 22-Apr-1995 #sequence_revision 26-May-1995 #text_change 20-Jun-2000 C;Accession: JX0368; PC2355; S68457; S78548 R;Saguchi, K.; Tobe, T.; Hashimoto, K.; Sano, Y.; Nakano, Y.; Miura, N.H.; J. Biochem. 117, 14-18, 1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B
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                                                                                                                                                                                                                                                                                                                                                            414 CLGFGFDVSYAFLE
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les 9; Conserv
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8; Conser
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207-211, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                               427
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Pred. No. 59;
1; Mismatches
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Pred. No. 21;
8; Mismatches
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                                                                                                                15-Oct-1999 #text_change 15-Oct-1999
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59;
                  W02C12.
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A;Gene: parE; NMA1941
C;Superfamily: DNA to
                                                                      A:Molecule type: DNA
A:Residues: 1-661 <PAR>
A:Cross-references: GB:AL162757;
      C; Keywords:
                                                          A: Experimental source:
                                                                                                                                        A; Reference number: A; Accession: C81822
                                                                                                                        A;Status: preliminary
                                                                                                                               A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491
A;Reference number: A81775; MUID:20222556
                                                                                                                                                                                          Nature 404,
                                                                                                                                                                                                                            C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                topoisomerase IV subunit B (EC 5.99.1.-) NMA1941 [imported] - Neisseria meningitidis
                                                                                                                                                                                                                   R;Parkhill, J.;
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                                                  Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Map position: 1
A; Introns: 14/2; 227/2; 337,
C; Superfamily: DNA-directed
                                                                                                                                                                                   Holroyd, S.; Jagels, K.
ature 404, 502-506, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Gene: CESP:F33H2.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A:Experimental source: clone F33H2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: EMBL: 281526;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-2144 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         submitted to the EMBL Data Library, November 1996
A;Reference number: Z19463
A;Accession: T21712
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 28.y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein F33H2.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Cottage,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DЪ
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A;Experimental source: strain Bristol N2; clone W02C12
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A:Accession: T25933
A:Status: preliminary: translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-1372 < MUR>
A:Residues: 1-1372 < MUR>
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                           5 YHLDV----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 YHLDVSLAFSEISVGAEFNKDDC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              l Similarity
10; Conserv
                                                                                                                                                                                          Achtman, M.; James, K.D.; Bent
Jagels, K.; Leather, S.; Moule,
topoisomerase (ATP-hydrolyzing) chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66/1; 774/2; 823/2; 1046/1; 1108/2; 1298/1
                                                                                                                                                                                                                                                                                                                                                                               -----SLAFSEISVGAEFNKDD
                                                       serogroup
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    337/3; 544/2; 626/3; 661/1; 776/1; cted DNA polymerase II
                                                                                                                                                                                                                                                                                                                                                                                                                                  31.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31.7%;
43.5%;
                                               GB:AL157959; NID:g7380371; PIDN:CAB85161.1; PID:g738
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                                                                                                                                                                                                                                                                                                                                                                                                            Score 46; DB 2; L
Pred. No. 1.4e+02;
4; Mismatches 7;
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Pred. No.
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                                                                                                                                                                                          Bentley, S.D.; oule, S.; Mungal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DВ
90;
                                                                                                                                                                                Mungall, K.; Quail,
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isomerase

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topoisomerase IV chain B NMB1682 [imported] - Neisseria meningitidis (strain MC58 serogration of Species: Neisseria meningitidis
C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C;Accession: D81055
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.R.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
Fi, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A;Authors: Agenome sequence of Neisseria meningitidis serogroup B strain Mc58.
A;Accession: D81055
A;Accession: D81055
A;Status: preliminary
A;Malonia Parental Mc58.
Search completed: January Job time: 69 sec
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C;Superfamily: DNA topoisomerase (ATP-hydrolyzing) chain B
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A;Residues: 1-661 <TET>
A;Cross-references: GB:AE002518; GB:AE002098; NID:g7226928; PIDN:AAF42030.1; PID:g722693
A;Experimental source: serogroup B, strain MC58
                                                                                                                                                                                                                                        Query Match 31.4
Best Local Similarity 34.5
Matches 10; Conservative
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34.5%; Pred. No. 49;
tive 5; Mismatches
                      6, 2002, 09:03:01
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YX99_BACHD
CYB_ASTPE
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PLO1_SCHPO
YJU6_YEAST
BU1B_MOUSE
PCK5_MOUSE
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KR11_YEAST
F13B_MOUSE
CFPA_TREPA
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CARBOHYDRATE-LINKAGE MEDLINE=20020247; Pu HOfsteenge J., Blomm "The four terminal c C-mannosylated on mu J. Biol. Chem. 274:3 -i- FUNCTION: C9 IS BE ADDED IN THE ABLE TO ENTER LII -i- PTM: THROMBIN CL -i- SIMILARITY: TO C -i- SIMILARITY: CONT -i- SIMILARITY: CONT		ENCE FINE-85 Ley K. Ley K. Seque J. 4: ENCE O INE-85 LENCE O INE-85 Lence O Lence O INE-85 Lence O Len	HUMAN 48; UL-198 EB-199 UG-200 LEMENT Sapie ryota; alia;	41. 41. 41. 41. 41. 41. 41. 41. 41. 41.
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InterPro; IPR000561; EGF-like.
InterPro; IPR001827; MAC_PERFORIN.
InterPro; IPR001862; MAC_PERFORIN.
InterPro; IPR001884; TSP_
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InterPro; IPR001884; MACPF; 1.
PFAm; PF00090; tsp_1; 1.
PFAM; PF00090; tsp_1; 1.
PFAM; PF00090; tsp_1; 1.
PFAM; SM00192; LDLa; 1.
SMART; SM00192; LDLa; 1.
SMART; SM00192; MACPF; 1.
SMART; SM00209; TSP1; 1.
SMART; SM00209; TSP1; 1.
PROSITE; PS00102; EGF 1; 1.
PROSITE; PS01209; LDLRA__; 1.
PROSITE; PS01209; LDLRA__; 1.
PROSITE; PS00199; MAC_PERFORIN; 1.
PROSITE; PS00199; MAC_PERFORIN; 1.
PROSITE; PS00199; MAC_PERFORIN; 1.
PROSITE; PS00199; TSP1; 1.
Complement pathway; Complement alteriplasma: Mambrana steptics.
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tack complex; Cytolysis; Transmembrane; Signal;
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MISSING (IN REF. 2).
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COMPLEMENT COMPONENT C9B.
COMPLEMENT COMPONENT C9B.
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LDL-RECEPTOR CLASS A.
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CLEAVAGE (BY THROMBIN).
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C9B
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RESULT 2
COS_HORSE STANDARD; PRT; 547
AC F48770;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 34, Created)
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 34, Created)
DT 01-FEC-1996 (Rel. 34, 
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
NCBI_TaxID=9796;
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POTENTIAL.

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EGF-LIKE.

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LDL-RECEPTOR CLASS
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attack

HSSP;

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Plasma; Membrane a
EGF-Like domain.
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CHAIN 26
CHAIN 26
CHAIN 26
CHAIN 26
CHAIN 314
TRANSMEM 314
TRANSMEM 335
DOMAIN 36
SITE 265
SITE 265
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Query Match Best Local s Matches 26

Similarity

Conservative

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Pfam; PF00090; tsp.1; 1.
PRINTS; PR00764; COMPLEMENTC9.
SMART; SM00192; LDLa; 1.
SMART; SM00457; MACPF; 1.
SMART; SM00209; TSP1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997
01-NOV-1997
20-AUG-2001
COMPLEMENT C
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Q62930;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lassiter H.A., Walz B.M., Wilson J.L., Jung E., Calisi C.R., Goldsmith L.J., Wilson R.A., Morgan B.P., Feldhoff R.C.; "The administration of complement component C9 enhances the survious of neonatal rats with Escherichia coli sepsis."; Pediatr. Res. 42:128-136(1997).

1- FUNCTION: C9 IS THE FINAL COMPONENT OF THE COMPLEMENT SYSTEM BE ADDED IN THE ASSEMBLY OF THE MEMBRANE ATTACK COMPLEX. IT I ABLE TO ENTER LIPID BILAYERS, FORMING TRANSMEMBRANE CHANNELS.

1- SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.

1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.

1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
PROSITE;
PROSITE;
PROSITE;
PROSITE;
                                                                                        PROSITE;
                                                                                                                                                                                                                                                                    InterPro; IPR000561; EGF-like.
InterPro; IPR002172; LDL_recept_A.
InterPro; IPR001862; MAC_perforin.
InterPro; IPR001884; TSP1.
Pfam; PF00057; ldl_recept_a; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restricted the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U49071;
HSSP; P01130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY;
MEDLINE-97355567; PubMed-9212048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       379
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                                           PS00022; EGF_1; 1.
PS01186; EGF_2; FALSE_NEG.
PS01209; LDLRA_1; 1.
PS50068; LDLRA_2; 1.
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7 (Rel. 35, Last sequence update)
1 (Rel. 40, Last annotation update)
COMPONENT C9 PRECURSOR.
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Rodentia;
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                     PERFORIN; 1
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Pred.
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N-LINKED (GLCNAC. ..) (POTENTIAL)

N-LINKED (GLCNAC. ..) (POTENTIAL)

N-LINKED (GLCNAC. ..) (POTENTIAL)

75E5FE961DE873B6 CRC64;
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No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              There are
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- cutstation
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RESULT 4
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CO Mammall
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RN SEQUEN
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Best Local
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Huesler T., Lockert D.H., Kaufman K.M., Sodetz J.M., Sims P.J.;

"Chimeras of human complement C9 reveal the site recognized by
complement regulatory protein CD59.";

J. Biol. Chem. 270:3483-3486(1995).

-i- FUNCTION: C9 IS THE FINAL COMPONENT OF THE COMPLEMENT SYSTEM
BE ADDED IN THE ASSEMBLY OF THE MEMBRANE ATTACK COMPLEX. IT I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CO9_RABIT STANDARD; PRT; 1948747; 01-FEB-1996 (Rel. 33, Created) 01-FEB-1996 (Rel. 33, Last sequence up 20-AUG-2001 (Rel. 40, Last annotation COMPLEMENT COMPONENT C9 PRECURSOR.
                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-s
                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
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SIGNAL 1
                                                                               or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND SEQUENCE OF 22-
STRAIN-NEW ZEALAND WHITE; TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryctolagus
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Plasma; Membrane at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=95181293; PubMed=7533152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9986;
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  U20055;
P01130;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Metazoa;
                                                                               email to license@isb-sib.ch).
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--- Chordata; Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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  AAC48459.1;
1AJJ.
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                                                                                                     license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lagomorpha;
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42.4%;
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POTENTIAL.
POTENTIAL.
EGF-LIKE.
CLEAVAGE (BY THROMBIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 59;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TSP TYPE-1
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is; Transmembrane; Sign
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryctolagus
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                                                                                                                                                                                 restrictions
                                                                                                                                   and
                                                                                                                                                                                                            EMBL
                                                                                                                                                                                                               a collaboration -
MBL outstation -
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InterPro; InterPro;

EGF-like

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RESULT 5
PPOL_ONCMA
ID PPOL_O
AC 008824
DT 01-OCT
DT 01-FEB
DT 20-AUG
DE POLY [
CONCORTH
OC EUKATY
OC PTOTAC
OX NCBI_T
RN SEQUEN
RX MEDLIN
RX MEDLIN
RA MIMAN
RA MIMAN
RA MIMAN
RA MIMAN
RT 1501
RF 011gon
RL BIOChe
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Best Local S
Matches 12
       "Isolation of cDNAs encoding the catalytic domain of poly(ADP-ribose) polymerase from Xenopus laevis and cherry salmon using heterologous oligonucleotide consensus sequences."; Blochem. Biophys. Res. Commun. 193:119-125(1993).
                                                                                                                                                                                                                                                                                                                                                                                                       POLLONCMA STANDARD; PRT; 135 AA. Q08824; O1-OCT-1994 (Rel. 30, Created) O1-FEB-1995 (Rel. 31, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) POLY (ADP-RIBOSE) POLYMERASE (EC 2.4.2.30) (P. POLY (ADP-RIBOSE) POLYMERASE (EC 2.4.2.30) (P. POLY (ADP-RIBOSE) POLYMERASE (EC 2.4.2.30) (P. POLYMERASE) (P.
                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE=93277538;
                                                                                                                                                                                                                                                        Oncorhynchus masou (Cherry salmon) (Masu salmon). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Onco
                                                                                                                                               Miwa M.;
                                                                                                                                                                                                                                                                                                                                                                                                  RIBOSYLTRANSFERASE)
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Pfam; PF01823; MACPF; 1
Pfam; PF00090; tsp_1; 1.
Pfam; PF00090; tsp_1; 1.
PRINTS; PF000764; COMPLEMENTC9.
SMART; SM00192; LDLa; 1.
SMART; SM00209; TSP1; 1.
PROSITE; PS00022; EGF 1; 1.
PROSITE; PS01186; EGF 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      384 KCLGFDLDLSLNIPGKSAGLSLTGQANKNNC 414
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasma; Membrane attack
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement pathway;
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12; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E; PS00022; EGF 1; 1.
E; PS01186; EGF 2; 1.
E; PS01209; LDLRA 1; 1.
E; PS00279; MAC_PEEFORIN; 1.
E; PS00279; MAC_PEFFORIN; 1.
                                                                                                                                                            Uchida K.,
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IPR002172;
IPR001862;
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                                                                                                                                               PubMed=8503897;
K., Uchida M., Ami
                                                                                                                                                                                                                                                                                                                                                                                   OLYMERASE (EC 2.4.2.30) (PARP) (POLY[ADP-RIBOSE] SYNTHETASE)
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; MAC_perforin.
; TSP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LDU-RECEPTOR CLASS A.
POTENTIAL.
POTENTIAL.
EGF-LIKE.
BY SIMILARITY.
OPOT N-LINKED (GLCNAC. . . ) (POT N-LINKED (GLCNAC. ) (POT N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 57; DB
Pred. No. 0.32
8; Mismatches
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                                                                                                                                            Kushida
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                                                                                                                                          s.,
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                                                                                                                                                                                                                                                        Oncorhynchus
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                                                                                                                                                                                                                                                                                                                                                                           (ADPRT) (NAD(+) (FRAGMENT).
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                                                                                                                                       0kada
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                                                                                                                                                                                                                                                                                                      Euteleostomi;
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RESULT 6
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2 CO9_MOUSE

2 P06683;

/T 01-JAN-1988 (Rel. 06, Created)

DT 01-JAN-1988 (Rel. 06, Last sequence update)

COMPLEMENT COMPONENT C9 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
Stanley K.K., Herz J.,
"Topological mapping of complement component c9 techniques suggests a novel mechanism for its in membranes.";
                                                         SEQUENCE FROM N.A. MEDLINE-88004404; PubMed-2443347;
                                                                                                          NCBI_TaxID=10090;
                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
ACT_SITE
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADP-ribosylation; Zinc-finger; Zinc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00347; PARP_ZN_FINGER_1; PARTIAL.
PROSITE; PS50064; PARP_ZN_FINGER_2; PARTIAL.
Transferase; Glycosyltransferase; NAD; DNA-b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001290;
InterPro; IPR001510;
Pfam; PF00644; PARP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; D13809; BAA02965.1; -. PIR; PN0494; PN0494.
                                                                                                                                                                                                                                                                                                                          11 LDIEVAYSLLKGGAEDNKKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P26446; 4PAX
                                                                                                                                                                                                                                                                                                                                          7 LDVSLAFSEISVGAEFNKDD
                                                                                                                                                                                                                                                                                                                                                                                                      Local
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MISCELLANBOUS: THE ADP-D-RIBOSYL GROUP OF NAD(+) IS TRANSFERRED TO AN ACCEPTOR CARBOXYL GROUP ON A HISTONE OR THE ENGYME ITSELF, AND FURTHER ADP-RIBOSYL GROUP ON A FIRANSFERRED TO THE 2'-POSITION OF THE TERMINAL ADENOSINE MOIETY, BUILDING UP A POLYMER WITH AN AVERAGE CHAIN LENGTH OF 20-30 UNITS.

SIMILARITY: BELONGS TO THE PARP FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: POLY(ADP-RIBOSE) POLYMERASE MODIFIES VARIOUS NUCLEAR PROTEINS BY POLY(ADP-RIBOSYL)ATION. THE MODIFICATION IS DEPENDENT ON DNA AND IS INVOLVED IN THE REGULATION OF VARIOUS IMPORTANT TUMOR TRANSFORMATION AND ALSO IN THE REGULATION, PROLIFERATION, AND EVENTS INVOLVED IN THE RECOVERY OF CELL FROM DNA DAMAGE.

CATALYTIC ACTYVITY: NAD(+) + (ADP-D-RIBOSYL)[N]-ACCEPTOR = NICOTINAMIDE + (ADP-D-RIBOSYL)[N]-ACCEPTOR.

COPACTOR: ZINC, CONTAINS TWO MOLES OF ZINC PER MOLE OF PROTEIN.

SUBCELLULAR LOCATION: NUCLEAR.

TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN OVARY, COCYTES,
                                                                                                                                                                                                                                                                                                                                                                                        l Similarity
10; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                         135
135
135 /
                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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135
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                                                                                                                     Rodentia;
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50.0%;
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                                                                                                        Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 1.3;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                         Score 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAD-BINDING
BY SIMILARI
                                                                                                                                                                                                                                                                                                                                                                                                                                              A60E8E98890E42DC CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAD; DNA-binding; Nuclear protein;
                                                                                                                                                                                       update)
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1.3;
            insertion
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                     by recombinant DNA
                                                                                                                                                                                                                                                                                                                                                                                                      Length 135;
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ntent is in
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RESULT 7
ITH4_HUMAN
ID ITH4_H
AC Q14624
DT 15-JUL
DT 20-AUG
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                                                                                                                                                                       δõ
                                                                                                                                       g
                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 10; Conser
 ITH4_HUMAN S
Q14624; Q15135; Q15-JUL-1998 (Rel
20-AUG-2001 (Rel
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DISULFID
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Pfam; PF00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00090; tsp_1; 1.
SMART; SM00192; LDLa; 1.
SMART; SM00457; MACPF; 1
SMART; SM00209; TSP1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000561; EGF-like.
InterPro; IPR002172; LDL_recept_A.
InterPro; IPR001862; MAC. perforin.
InterPro; IPR000884; TSP1.
                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complement pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute.
                                                                                                                                       358
                                                                                                                                                                       Ν
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O J. 6:1951-1957(1987).

FUNCTION: C9 IS THE FINAL COMPONENT OF THE COMPLEMENT SYSTEM TO BE ADDED IN THE ASSEMBLY OF THE MEMBRANE ATTACK COMPLEX. IT IS ABLE TO ENTER LIPID BILAYERS, FORMING TRANSMEMBRANE CHANNELS. SIMILARITY: TO COMPLEMENT FACTORS C6, C7, C8, AND TO PERFORIN. SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.

SIMILARITY: CONTAINS 1 LDL-RECEPTOR CLASS A DOMAIN.

SIMILARITY: CONTAINS 1 LDL-RECEPTOR CLASS A DOMAIN.
                                                                                                                                       CLGFNMDLRIPLQDDLKDASVTASVNADGC
                                                                                                                                                                    CLGYHLDVSLA----FSEISVGAEFNKDDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGI:1098282; C9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through the Swiss Institute of Bioinformatics and the EN
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PF01823; MACPF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X05475; CAA29038.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PS01186;
PS01209;
PS50068;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PS50092; TSP1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PS01209; LDLRA_1; 1.
PS50068; LDLRA_2; 1.
PS00279; MAC_PERFORIN;
                                                                                                                                                                                                                                                                                        243
397
528
 (Rel. 36, Created)
(Rel. 40, Last seq
                                                                                                                                                                                                                                                                                                                                           292
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                                                                                                                                                                                                       Conservative
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                                                   STANDARD;
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                                 090054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       attack
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EGF_2; FALSE_NEG
                                                                                                                                                                                                                                                                                                           1114
308
332
523
523
112
112
387
5511
522
243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complement alternate pathway; Glycoprotein;
tack complex; Cytolysis; Transmembrane;
                                                                                                                                                                                                                      33.8%;
                                                                                                                                                                                                                                                                                             60020
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 sequence update
                                                                                                                                                                                                  Score 49; DB Pred. No. 5.3; 6; Mismatches
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POTENTIAL.
POTENTIAL.
EGF-LIKE.
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5.3;
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EMBL;
                                                                                                                               use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no restude by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Choi-Miura N.-H., Sano Y., Oda E.,
Taniyama M., Katagiri T., Tomita M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-96389995; Pubm
Saguchi K., Tobe T., H
Miura N.H., Tomita M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "cDNA and deduced amino acid sequence kallikrein-sensitive glycoprotein."; FEBS Lett. 357:207-211(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-AUG-2001 (Rel. 40, Last annotation update)
INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H4 PRECURSOR (ITI HEAVY
CHAIN H4) (INTER-ALPHA-TRYPSIN INHIBITOR FAMILY HEAVY CHAIN-RELATED
PROTEIN) (HERP) (PLASMA KALLIKREIN SENSITIVE GLYCOPROTEIN 120) (PK-
120) (GP120) [CONTAINS: GP57].
ITIH4 OR IHEP OR ITIHL1 OR PK120.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=95332266; PubMed=7541790;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-P]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    plasma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=95293915; PubMed=7775381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PARTIAL SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  inhibitor family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 *Isolation and characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nagasawa S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nishimura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=95104473;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inhibitor family heavy chain-related protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Cloning and characterization of cDNA for inter-alpha-trypsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     romita M.;
                                                                                                                                                                                                                                                           PTM: APPEARS TO BE BOTH N- AND O-GL SIMILARITY: BELONGS TO THE ITIH FAM SIMILARITY: CONTAINS 1 VWFA DOMAIN.
                                                                                                                                                                                                                                                                                                                                              AFTER DIFFERENT SURGICAL TRAUMA.
PTM: CLEAVED BY PLASMA KALLIKREIN TO
                                                                                                                                                                                                                                                                                                               FRAGMENTS, AND THE RESULTING TO A 70-KDA FRAGMENT.
D38595;
D38535;
U43163;
U42015;
U42016;
U43155;
U43156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               glycoprotein.";
chem. 117:14-18(1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amily heavy chain-related 119:898-905(1996).
               AAD05198.1;
AAD05198.1;
AAD05198.1;
                                                               BAA07602.1;
BAA07536.1;
AAD05198.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tobe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=8797089;
T., Hashimoto K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AND CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=7805892;
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JOINED.
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                                                                                                                                                                                                                                                                              AND O-GLYCOSYLATED. ITIH FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of the human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nakano Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sasaki N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of human PK-120, a
                                                                                                                                             (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sano
                                                                                                                                                                                                                                                                                                                                                                                                                                                               novel glycoprotein which inter-alpha-trypsin inhib
                                                                                                                                                                                                                                                                                                                                                 YIELD
                                                                                                                                                                                                                                                                                                                                  FRAGMENT
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                                                                                                                                                                Usage
                                                                                                                                                                                                                                                                                                                                                                                  IN THE SERA
                                                                                                                                                                                                                                                                                                                                                                                                                   REACTIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           inter-alpha-trypsin
(IHRP) gene (ITIHL1).";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tobe T., Yanagishita
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                                                                                                                                                                                                                                                                                                                                                 100- AND
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                                                                                                                                                                                                              EMBL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inhibitor
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                                                                                                                                                                                                                  collaboration -
                                                                                                                                                                                                              outstation
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RESULT MOAEL SY ID MOAEL SY ID MOAEL SY ID MOAEL SY ID TO 15 ID TO
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Best Local s
Matches s
                                   SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SUBDIT L.M., Flores E., Herrero A.;

Submitted (ANG-1996) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: CONVERSION OF MOLYBDOPTERIN PRECURSOR Z INTO

MOLYBDOPTERIN REQUIRES TRANSFER OF TWO SULFUR ATOMS TO PRECURSOR

(TO GENERATE THE DITHICLENE GROUP). THIS IS CATALYZED BY THE

CONVERTING FACTOR COMPOSED OF A SMALL AND LARGE SUBUNIT (BY
                                                                                                                                                                                                                                                              Q56210;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
MOLYBDOPTERIN [MPT] CONVERTING FACTOR, SUBUNIT 2 (BIOSYNTHESIS PROTEIN E) (MOLYBDOPTERIN CONVERTING
                                 -<u>'</u>-
                                                                                                                                                                                                                                                                                                                                                                                                                       _SYNP7
                                                                                                                                                                                                                Synechococcus sp. (strain Bacteria; Cyanobacteria; C
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CARBOHYD
DISULFID
DISULFID
CONFLICT
                                                                                                                                                                                                     NCBI_TaxID=1140;
                                                                                                                                                                                                                                                                                                                                                                                                    MOAE_SYNP7
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CARBOHYD
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CARBOHYD
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SIGNAL
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SMART; SM00327; VWA; 1.
PROSITE; PS50234; VWFA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
EMBL;
EMBL;
EMBL;
SIMILARITY).

PATHWAY: MOLYBDENUM COFACTOR BIOSYNTHESIS SUBUNIT: HETERODIMER OF MOAD AND MOAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002035; vWFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 CLGYHLDVSLAFSE 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    600564;
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U43158; AAD05198.1;
U43159; AAD05198.1;
U43160; AAD05198.1;
U43161; AAD05198.1;
U43162; AAD05198.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      816
930
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207
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661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31.7%;
                                                                                                                                                                                                       n PCC 7942) (Anacystis nidulans R2).
Chroococcales; Synechococcus.
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JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 46; DB;
Pred. No. 28;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROBABLE.

N -> I (IN REF. 2).

N -> K (IN REF. 3).

S -> N (IN REF. 4).

O -> E (IN REF. 4).

O -> V (IN REF. 4).
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N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
O-LINKED (GLCNAC.
O-LINKED (GLCNAC.
O-LINKED (GLCNAC.
O-LINKED (GLCNAC.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70 KDA INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H4.
POTENTIALLY ACTIVE PEPTIDE.
35 KDA INTER-ALPHA-TRYPSIN INHIBITOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-LINKED
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0E1929065F4EB6A0 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Signal; Multigene
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GLCNAC . . . )
GLCNAC . . . )
GLCNAC . . . )
GLCNAC . . . )
GLCNAC (PROB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 REF
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(POTENTIAL).
(POBABLE).
(PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 930;
                                                                                                                                                                                                                                                                                         (MOLYBDENUM COFACTOR
                                                                                                                                                                                                                                                                            FACTOR LARGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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D7 01-OCT

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Best Local s
Matches 10
EMBL; L10667; AAA34727.1;
EMBL; Z72951; CAA97191.1;
PIR; S30784; S30784.
PIR; S42158; S42158.
                                                                                                                                                            This SWISS.PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                    MEDLINE-97435481; PubMed=9290212;
Rieger M., Brueckner M., Schaefer M., Mueller-Auer S.;
Rieger M., Brueckner M., Schaefer M., Mueller-Auer S.;
Requence analysis of 203 kilobases from Saccharomyces cerevisiae chromosome VII.";
Yeast 13:1077-1090(1997).
-i- FUNCTION: INVOLVED IN CELL WALL (1-->6)-BETA-GLUCAN SYNTHESIS.
KREI IN THE BIOSYNTHESIS OF BETA-1,6-GLUCANS.
-i- RATHWAY: BIOSYNTHESIS OF BETA-1,6-GLUCANS.
-i- SUBCELLULAR LOCATION: CYTOPLASMIC.
                                                                                                                                        or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN=S288C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brown J.L., Kossaczka Z., Jiang B., Bussey H., A mutational analysis of killer toxin resistance in Saccharomyces cerevisiae identifies new genes involved in cell wall (1-->6)-beta-glucan synthesis. Genetics 133:837-849(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=93216084; PubMed=8462845; MEDLINE=93216084; PubMed=8462845; Miang B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1993
01-OCT-1993
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-007-1993 (Rel. 27, Last Sequence up 01-NOV-1997 (Rel. 35, Last annotation BETA-GLUCAN SYNTHESIS-ASSOCIATED PROTER RESISTANCE PROTEIN 11).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=4932;
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P32893;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                  and this statement is not removed requires a license agreement (See an email to license@isb-sib.ch).
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18712 MW; AC016984E1D587FB CRC64;
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Pred. No. 9.8;
5; Mismatches
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RESULT 10
F13B_MOUSE
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Best Local
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01-FEB-1995 (Rel. 31
01-FEB-1995 (Rel. 31
20-AUG-2001 (Rel. 40
COAGULATION FACTOR )
                                                                                                                                                                                       Transferase;
Sushi.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-93224141; PubMed-8468048; Monaka M., Matsuda Y., Shiroishi 'Natsuume-Sakai S.; Molecular -
                                          CHAIN
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or send a
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Cell wall.
SEQUENCE 560 AA; 6
  DOMAIN
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Molecular cloning of the b subunit of mouse coagulation factor XIII and assignment of the gene to chromosome I: close evolutionary relationship to complement factor H.";

Genomics 15:535-542(1993).

Genomics 15:535-542(1993).

FORMATION EXILITS NOT CATALYTICALLY ACTIVE.

BUT IS THOUGHT TO STABILIZE THE A SUBUNITS AND REGULATE THE RATE

OF TRANSGLUTAMINASE FORMATION BY THROMBIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-FEB-1995 (Rel. 31, Last sequence update)
20-AIG-2001 (Rel. 40, Last annotation update)
COAGULATION FACTOR XIII B CHAIN PRECURSOR (EC 2.3.2.13) (PROTEIN-
GLUTAMINE GAMMA-GLUTAMYLTRANSFERASE B CHAIN) (TRANSGLUTAMINASE B
                                                                                                                                                                                                                                                                                                            MGD; MGI:88379; F13b.
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                                                                                                                                                                                                                                                   SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         modified
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non-profit institutions as long
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                                                                                                                                                                                                                               Plasma;
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Rodentia;
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Blood
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                                                                                                                                                                                                                           coagulation; Repeat; Glycoprotein;
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                                                                                                                                                                    FACTOR
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RESULT 11.

CFPA_TREPA STANDARD; PRT; (
AC Q56336;
DT 15-DEC-1998 (Rel. 37, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence up
DT 30-AUG-2001 (Rel. 40, Last annotation
DE CYTOPLASMIC FILAMENT PROTEIN A.
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STRAIN. MICHOLS;
STRAIN. MICHOLS;
STRAIN. MICHOLS;
STRAIN. MICHOLS;
STRAIN. MICHOLS;
Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
Fraser C.M., Norris S.J., Weinstock G.M., White O., Setchum K.A.,
Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
Dodson R., Gwinn M., McLeod M.P., Saliberg S., Peterson J.,
Sodergren E., Hardham J.M., McLeod M.P., Saliberg S., Peterson J.,
Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,
McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S.
McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S.
McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Smith H.O.,
McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Smith H.O.,
McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Smith H.O.,
McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Smith H.O.,
McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Smith H.O.,
McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Smith H.O.,
McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S.
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DISULFID
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SEQUENCE
                                 spirochete.";
Science 281:3
                                                                                                                                                                                                                                                                                       "Characterization of the cytoplasmic Treponema pallidum subsp. pallidum."; Bacteriol. 178:3177-3187(1996).
                                                                                                                                                                                                                                                                                                                                                            MEDLINE=96236033; PubMed=8655496; You Y., Elmore S., Colton L.L., M
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Treponema pallidum.
Bacteria; Spirochaetales;
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11; Conser
281:375-388(1998).
CTION: COMPONENT OF
GTH OF THE ORGANISM
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BY SIMILARITY.
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Pred. No. 41;
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Matches 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBO J. 14:610-618(1995).

-i- FUNCTION: COULD BE INVOLVED IN THE CONVERSION OF SUGARS, WHICH ARE A MAJOR PHENOMENON IN THE REHYDRATION PROCESS.

-i- CATALYTIC ACTIVITY: SEDCHEPTULOSE 7-PHOSPHATE + D-GLYCERALDEHYDE -1- CAPALYTIC ACTIVITY: SEDCHEPTULOSE 7-PHOSPHATE + D-STACTOR: THIAMINE PYROPHOSPHATE.

-i- COPACTOR: THIAMINE PYROPHOSPHATE.

-i- TISSUE SPECIFICITY: LEAVES.

-i- TISSUE SPECIFICITY: LEAVES.

-i- SIMILARITY: BELONGS TO THE TRANSKETOLASE FAMILY.
                                                                                                                                                                                                                                                                                                           Bernacchia G., Schwall G., Lottspeich F., Salamini F., Bartels "The transketolase gene family of the resurrection plant Craterostigma plantagineum: differential expression during the
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE=95163594; PubMed=7859749;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Craterostigma plantagineum.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Lamiales; Lamiales incertae sedis; Torenieae;
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VW; 7F77A144214B7948 CRC64;
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Pred. No. 41;
6; Mismatches
                  (See http://www.isb-sib.ch/announce/
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41;
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                                                                                                                                                                                                       Glycoprotein; Transmembrane; SIGNAL 2
                                                                                                                                                                                                                                                     EMBL; L25706; AAA43831.1; -
                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content entities requires a license agreement (See http://www.isb-orsend an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                 between the Swiss Institute of Bioinformatics Institute
                                                                                                                                                                                                                                                                                                                                                 Virology 202:173-185(1994).
-!- SIMILARITY: BELONGS TO THE HERPESVIRUSES GLYCOPROTEIN B FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                 Schleiss M.R.; "Cloning and characterization of the guinea pig cytomegalovirus
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE=94279138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Guinea pig cytomegalovirus (strain 22122 / ATCC VR682) (GPCMV). Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VGLB_GPCMV STANDARD; PRT; 901 AA. 069024; 15-DEC-1998 (Rel. 37, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Betaherpesvirinae; Muromegalovirus
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Pfam; PF00456; transketolase; 1
PROSITE; PS00801; TRANSKETCLASE_1; 1.
PROSITE; PS00802; TRANSKETCLASE_2; 1
Transferase; Thiamine pyrophosphate; Multigene family.
SEQUENCE 679 AA; 73130 MW; 1109092E136A345B CRC64;
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HSSP; P23254; 1AY0.
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3; Mismatches
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ID YG5X_YEAST
AC P53336;
DT 01-0CT-1996
DT 01-0CT-1997
DE HYPOTHETICAL
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              01-OCT-1996
01-OCT-1996
01-NOV-1997
                                                                                                                                                                                                                                               DNA_BIND
SEQUENCE
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Submitted (OCT-1994) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).
-!- SUBLIARITY: CONTAINS 1 ZN(2)-CYS(6), FUNGAL-TYPE BINUCLEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
PUTATIVE 107.6 KDA TRANSCRIPTIONAL REGULATORY
                                                                                                                                                                                                                                                                                                                            SGD; S0004541; YML076C.
InterPro; IPR001138; Zn2_CY6_fungal.
SMART; SM00066; GAL4; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                  EMBL;
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  HYPOTHETICAL
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                                                                                                                                                                                                                                                 107560 MW;
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PROTEIN IN BGL2-ZUO1 INTERGENIC REGION.
                                                                                                                                                                                Score 44; DB Pred. No. 58; 6; Mismatches
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                                                                                                                                                                                                                                               ZN(2)-CYS(6), FUNGAL-TYPE 020A56745DF52CCC CRC64
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Pred. No.
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FALSE_NEG.
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                                                                                                                                                                                                                                                                                                                                                                                                                   Volckaert G., Voet M., Robben J.;
"Sequence analysis of a near-subtelomeric 35.4 kb DNA segment on the right arm of chromosome VII from Saccharomyces cerevisiae carrying the MALI locus reveals 15 complete open reading frames, including ZUO1, BGL2 and BIO2 genes and an ABC transporter gene.";
Yeast 13:251-259(1997).
                                                                                                                                                  Hypothetical SEQUENCE 3
                                                                                                                                                                            InterPro; IPR003750; DUF171. Pfam; PF02598; DUF171; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A
STRAIN=S288C / FY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                  EMBL; 273068; CAA97314.1; -. SGD; S0003515; YGR283C.
                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97245295; PubMed=9090054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae (Baker's yeast).
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 216
                                1 KCLGYHLDVSLAFSEISVG-----AEFNKDD
KPLGYHVRMASTLNEVSEGYTKIVWVNSGDFHYDE
                                                                                 Similarity
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                                                                   Conservative
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Maximum Match 100%
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 SPTREMBL_17:*

1: sp_archea:*
2: sp_bacteria
3: sp_fungl:*
4: sp_human:
5: sp_human:
6: sp_namma
7: sp_mac;
8: sp_oxg
9: sp_ph
10: sp_r
11: sp_1
12: ss
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Gapop 10.0 , Gapext 0.5
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sp_organelle:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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MEDITINE-95258030; PubMed=9595666; Cooke S.J., Jolley K., Ison C.A., Young H., Heckels J.E.; "Naturally occurring isolates of Neisseria gonorrhoeae, which display anomalous serovar properties, express PIA/PIB hybrid porins, deletions
                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-1998 (TremBLrel. 06, Created)
01-JUN-1998 (TremBLrel. 06, Last sec
01-JUN-2001 (TremBLrel. 17, Last and
OUTER MEMBRANE PROTEIN I PRECURSOR.
                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN=1702;
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051948;
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Bacteria; Proteobacteria;
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SEQUENCE
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J. Clin. Microbiol. 38:4430-4438(2000).

-i- SUBBUIT: HOMOTRIMER (BY SIMILARITY).

-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9E231;
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Q1-MAR-2001 (TrEMBLrel. 16,
Q1-JUN-2001 (TrEMBLrel. 17,
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Bacteria; Proteobacteria;
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                                                                                                                                                                                                                                                                                         Neisseriaceae; Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 567;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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RESULT
051944
ID 05
AC 05
DT 01
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Best Local S
Matches 10
     051944
051944;
01-JUN-1998
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9Z4K1, PRELIMINARY,
Q9Z4K1;
01-MAY-1999 (TrEMBLrel. 1
01-MAY-1999 (TrEMBLrel. 1
01-JUN-2001 (TrEMBLrel. 1
                                                                                                                                                                                                                               InterPro; IPR001702; Gram_neg_porin.
Pfam; PF00267; Gram_ve_porins; 1.
PRINTS; PR00182; ECOLNEIFORIN.
PROSITE; PS00576; GRAM_NEG_PORIN; 1.
Outer membrane; Porin; Signal; Transmembrane.
SIGNAL 1 19
POTENTIAL.
                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                      Submitted (SEP-1998) to the EMBL/GenBank/DDBJ-!- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                   (BY SIMILARITY).
EMBL; AF090824; AAC79493.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                             Fudyk T.C., Maclean I.W., Brunham R.C., Plummer F.A.
                                                                                                                                                                                                                                                                                                                                                                                       gonorrhoeae.
                                                                                                                                                                                                                                                                                                                                                                                       "Genetic Diversity and Mosaicism conorrhoeae.":
                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-4846;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neisseria gonorrhoeae.
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OUTER MEMBRANE PROTEIN
                                                                                                                                                           Local Similarity
                                                                                                         1 KCLGYHLDVSLAFSEISVGAEFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
SEQUENCE
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FEMS Microbiol Lett 162:75-82(1998).
-!- SUBGUIT: HOMOTRIMER (BY SIMILARITY)
-!- SUBCELULAR LOCATION: INTEGRAL MEMBR
(BY SIMILARITY)
EMBL; AF015122; AAC38568.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001702; Gram_neg_porin.
Pfam; PF00267; Gram-ve_porins; 1.
PRINTS; PR00182; ECOLNEIPORIN.
PROSITE; PS00576; GRAM_NEG_PORIN; 1.
Outer membrane; Porin; Signal; Transmembrane.
SIGNAL 1 19
                                                           G
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                                                                                          KGLVYHADLSNDYDQVVVGAEYD 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 KCLGYHLDVSLAFSEISVGAEFN 23
                                                                                                                                                   10;
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326 AA;
    (TrEMBLrel.
                             PRELIMINARY;
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nilarity 43.5%;
Conservative
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; 35611 MW;
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43.5%;
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; 35558 MW;
    06,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10, Created)
10, Last sequence update)
17, Last annotation updat
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Created)
                                                                                                                                         Score 52; DB
Pred. No. 6.2;
6; Mismatches
                                                                                                                                             6;
                                                                                                                                                                                                     POTENTIAL.
OUTER MEMBRANE PROTEIN
; 5F0CC17B6A8FA323 CRC6
                                                                                                                   23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE
                           PRT;
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Pred. No. 6.
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; 3D566D777D7CA015 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                         326
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6.2;
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6.2;
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                                                                                                                                                                  Length 326;
                                                                                                                                                                                                         CRC64;
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                                                                                                                                        Indels
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RESULT
Q9Z4L5
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EMBL; AF090823; AAC39492.1; -.

InterPro; IPR001702; Gram_neg_porin.

Pfam; PF00267; Gram_ve_porins; 1.

PRINTS; PR00182; ECOLNEIPORIN.

PROSITE; PS00576; GRAM_NEG_PORIN; 1.

POUTER membrane; Porin; Signal; Transmembrane.

I SIGNAL 1

1 19

POTENTIAL.
                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                   Matches
                             Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases -:- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
-:- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-1998 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
OUTER MEMBRANE PROTEIN
                                                                            Fudyk T.C., Maclean I.W.,
Brunham R.C., Plummer F.A.
                                                                                                                                   Neisseria gonorrhoeae.
Bacteria; Proteobacteria;
                                                                                                                                                                         01-MAY-1999
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (SEP-1998) to the EMBL/Ge-i-SUBUNIT: HOMOTRIMER (BY SIMILAR-i-SUBCELLULAR LOCATION: INTEGRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fudyk T.C., Maclean I.W.,
Brunham R.C., Plummer F.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cooke S.J., Jolley K., Ison C.A., Young H., He "Naturally occurring isolates of Neisseria gon anomalous serovar properties, express PIA/PIB in PIB or novel PIA molecules.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-1998
01-JUN-2001
 InterPro;
           EMBL;
                                                        gonorrhoeae."
                                                                  "Genetic Diversity and
                                                                                              STRAIN-4266;
                                                                                                       SEQUENCE FROM N.A.
                                                                                                                        NCBI_TaxID=485;
                                                                                                                                                                OUTER MEMBRANE
                                                                                                                                                                                            01-MAY-1999
                                                                                                                                                                                                      Q9Z4L5;
                                                                                                                                                                                                               Q9Z4L5
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gonorrhoeae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEMS Microbiol. Lett. 162:75-82(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=98258030; PubMed=9595666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Genetic Diversity and
                                                                                                                                                                                                                                                              268 KGLVYHADLSNDYDQVVVGAEYD
                                                                                                                                                                                                                                                                               1 KCLGYHLDVSLAFSEISVGAEFN
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          (BY SIMILARITY); AF090808; AAC
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                                                                                                                                                                                                                                                                                                            Similarity
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Proteobacteria;
 IPR001702;
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326 AA;
                                                                                                                                                                        (TrEMBLrel.
                                                                                                                                                                                            (TrEMBLrel.
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                                                                                                                                                                                                               PRELIMINARY;
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         AAC79477.1;
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35577 MW;
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Gram_neg_porin.
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                                                                   Mosaicism
                                                                                                                                                                 10, Created)
10, Last sequence update)
17, Last annotation updat
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17, Last annotation update)
                                                                                                                                                               PRECURSOR.
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                                                                                                                                   beta
                                                                                    Simonsen J.N.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  beta subdivision; Neisseriaceae; Neisseria
                                                                                                                                                                                                                                                                                                  6
                                                                                                                                                                                                                                                                                                  Score 52; DB
Pred. No. 6.2;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                 OUTER MEMBRANE PROTEIN I. BF50F03EAF73BEE4 CRC64;
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                                                                                                                                                                                                                                                              290
                                                                                                                                                                                                               PRT;
                                                                                                                                   subdivision;
                                                                  at
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                                                                                    Njagi E.N.,
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gonorrhoeae, which display
PIB hybrid porins, deletions
                                                                                                                                   Neisseriaceae; Neisseria
                                                                  locus
                             PROTEIN. OUTER
                                                                                                                                                                        update)
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RESULT
Q917L2
ID Q9
AC Q9
AC Q9
DT 01
DT 01
DT 01
DT 02
DE CC
GN CC
GN CC
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013834
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Best Local
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Best Local (
                                                                                                                                                                                                                                                                                                                                                          Wood V., Barrell B.G., Rajandream M.A. Submitted (SEP-1997) to the EMBL/GenBa EMBL; Z99531; CAB16714.1; -. InterPro; IPR000569; HECT.
InterPro; IPR001000; Glyco_hydro_10.
InterPro; IPR001345; PG_mutase.
Pfam; PF00632; HECT; 1.
            Q917L2
Q917L2;
01-MAR-2001 (TrE
01-MAR-2001 (TrE
01-JUN-2001 (TrE
CG3066 PROTEIN
CG3066
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013834;
01-JAN-1998
01-JAN-1998
01-JUN-2001
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PRINTS; PR00182; ECOLNEIPORIN.
PROSITE; P800576; GRAM_NEG_PORIN; 1.
PROSITE; P800576; GRAM_NEG_PORIN; 1.
Outer membrane; Porin; Signal; Transmembrane.
SIGNAL 1 19 POTENTIAL.
CHAIN 20 327 OUTER MEMBRANE F
                                                                                                                                                                   1339
                                                                                                                                                                                                                                                                                         SMART; SM
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UBIQUITIN SYSTEM PROTEIN SPAC19D5.04.
                                                                                                                                                                                                                                                                                                                   PROSITE; PS00591; GLYCOSYL_HYDROL_F10; UNKNOWN_1.
PROSITE; PS50237; HECT; 1.
PROSITE; PS00175; PG_MUTASE; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Devlin K., Churcher C.M.; Submitted (SEP-1997) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=972H-;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schizosaccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schizosaccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=972H-;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               269 KGLVYHADLSNDYDQVVVGAEYD
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                                                                                                                                                                                            2 CLGYHLDVSLAFSEISVGAEFNKDDC
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                                                                                                                                                                CILYLLEVLLADSKKPDEFEFNSEDC 1364
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                                                                                                                                                                                                                      Similarity
12; Conserv
                                                                                                                                                                                                                                                                                                         SM00119;
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327 1
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L (TrEMBLrel.
L (TrEMBLrel.
                                                                                                                                                                                                                                                                                           3227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel. 05, (TrEMBLrel. 17,
                                                                                                                                                                                                                       Conservative
                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AΑ;
                                                                                                                                                                                                                                                                                           AΑ;
                                                                                                                                                                                                                                                                                                         HECTC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        327 (
35471 MW;
                                                                                                                                                                                                                                 35.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35.9%;
                                                                                                                                                                                                                                                                                           365031
                                         16,
17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schizosaccharomycetaceae;
                                      Created)
Last sequ
Last anno
                                                                                                                                                                                                                   Score 52; DB Pred. No. 80; 4; Mismatches
                                                                                                                                                                                                                                                                                           MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                    4;
                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 52; DB Pred. No. 6.3; 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OUTER MEMBRANE PROTEIN I. FDB0D0FE8E53E32F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               291
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                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                            27
                                        sequence update)
annotation update)
                                                                                                                                                                                                                                                                                           07FC47AB79124575 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                             .A.;
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                                                                                              241
                                                                                                                                                                                                                                DB
80;
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3;
                                                                                              AΑ
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                                                                                                                                                                                                                       10;
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                                                                                                                                                                                                                                                Length 3227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                       0,
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0,

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RESULT
Q9SSX1
ID Q9
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                                                                                                                                QΥ
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RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Ballew R.M., Bay A. R., Yandell M.D., Zhang Q., Chen L.X.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Bay A. A. A. H.-J., Andrews Pfannkoch C., Bladwin D.,
RA Besson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Blazen A., Batter H., Caddeu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugar-Rocha S., Dunkov B.C., Dunkov B.C., Dowley S., Davley S., Dahlke C., Davenport L.B., Davies P.,
RA Bolos B., Delcher A., Deng Z., Mays A.D., Dow I., Dietz S.M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernadez J.R., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Hernadez J.R., Houck J.,
RA Harris N.L., Malush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Liu X., Mattei B., McIntosh T.C., McIecod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Wang Z.-Y., Wassaman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassaman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassaman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassaman D.A., Weinstock G.M., Weissenbach J.,
RA Wang S.A., Weinstock G.M., Weinstock G.M., Stup G., Zhao Q., Zheng Y.H., Wang X.H., Wang X.H.,
RA Shue B.C., Siden-Kiamos T., Shan M., Zhang G., Zhao 
                                                                                                                                                                     Matches
                                                                                                                                                                                        Query Match
Best Local
 Q9SSX1
                                                                                                                                                                                                                                                                             PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                        PIAM: PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00089;
                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Trypsin.
                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE003676; AAG22127.1; -- FlyBase; FBgn0037515; CG3066.
                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: TO SERINE PROTEASES, TRYPSIN FAMILY
                                                                                                   168
                                                                                                                                                                                    Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20196006; PubMed=10731132;
                                                9
                                                                                        NIHLISSQLCVGGEFYRDSC 187
                                                                                                               DVSLAFSEISVGAEFNKDDC
                                                                                                                                                                   Similarity
8; Conserv
                                                                                                                                                                                                                                                 Serine protease
241 AA; 27002 MW;
   PRELIMINARY;
                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
a; Drosophilidae; Drosophila.
                                                                                                                                                                         32.4%;
                                                                                                                            27
                                                                                                                                                      Score 47; DB Pred. No. 27; 5; Mismatches
   PRT;
                                                                                                                                                                                                                                       A4A0228330F64C1E CRC64;
 278
ΑA
                                                                                                                                                                                          5;
                                                                                                                                                      7;
                                                                                                                                                                                      Length 241;
                                                                                                                                                                                                                                                                                                                                                                                                                                     FAMILY
                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  (S1).
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Q9V3Z2
ID Q9
AC Q9
DT 01
DT 01
DT 01
DT 01
DT CG
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Q9SNG2
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Best Local
                                                                                                                                                 Matches
Q9V3Z2; PRELIMINARY,
Q9Y3Z2;
01-MAY-2000 (TrEMBLrel. 1
01-MAY-2000 (TrEMBLrel. 1
01-JUN-2001 (TrEMBLrel. 1
CG3066 PROTEIN.
CG3066.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                EMBL; APC
SEQUENCE
                                                                                                                                                                                                      Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                         Q9SNG2 PRELIMINARY; PRT; 367 AA.
Q9SNG2;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-MAY-2000 (TrEMBLrel. 13, Last annotation update)
EST C72179(E1153) CORRESPONDS TO A REGION OF THE PREDICTED GENE.
                                                                                                           235
                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9SSX1;
01-MAY-2000
01-MAY-2000
01-JUN-2001
                                                                             11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99430869; PubMed=10503544;
Takeda Y., Hatano S., Sentoku N., Mats
"Homologs of animal eyes absent (eya)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta;
Spermatophyta; Magnoliophyta; Liliopsid;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                      1 KCLGYHLDVSLAFSEISVGAEFNKDDC
                                                                                                                                                                                                                                                                                                                                                                                                                                  202 KCLLYRLDDVVAFENVYSSWEVGKLQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mol. Gen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OSEYAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity nes 11; Conser
                                                                                                                                                                                                                                                                                                                                                                                                           10
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 KCLGYHLDVSLAFSEISVGAEFNKDDC
                                                                                                    KCLLYRLDDVVAFENVYSSWEVGKLQC 261
                                                                                                                                                                                               tted (OCT-1999) to the EMBL/GenBank/DDBJ databases AP000616; BAA85447.1; -. NCE 367 AA; 42367 MW; FF9F290nF82F277F CTGA
                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gen. Genet. 262:131-138(1999).
AB028887; BAA85161.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            278 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                            ĀΑ;
                                                                                                                                                                                            42367 MW;
                                                                                                                                                      32.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31844 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32.4%;
               13,
13,
17,
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13,
17,
                       Created)
            Last sequence up
                                                                                                                                       Pred. No. 42;
2; Mismatches
                                                                                                                                                              Score 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 47;
Pred. No.
                                                                                                                                                                                        FF9F290DE82F273E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7BC1E2C41343B7A1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             eptophyta; Embryophyta; Tracheophyta;
Liliopsida; Poales; Poaceae;
                                                                                                                        27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                   228
                                                                                                                                                                                                                                                                                                                                                                                                                                                      27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matsuoka
                                                     391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DВ
31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genes
                                                                                                                                                             DB 10;
                                                   ΑA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10;
                                                                                                                                          14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           are found in higher
                                                                                                                                                           Length 367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                              6
                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                     Gaps
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                                                                                                                                    0;
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Batlew R.M., Basu A., Baxer E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfeinnkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendaie J., Bayraktaroglu L., Beasley E.M.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Gerry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Gebart W.M., Galsser R.,
RA Gebart S., Dunkov B.C., Davenport L.B., Dietz S.M.,
RA Gebart S., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Gebart S., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Gebart S., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Gebart S., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Gebart W., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Gebart W., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.I., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.I., Harvey D., Helman T.J., Wein M.-H., Diegwam C.,
RA Harris N.I., Harvey D., Helman T.J., Wein M.-H., Degwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kraytlz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kraytlz S., Kulp D., Lai Z.,
RA Harris N.I., Mandra R., Nixon K., Nusskern D.R., Moshrefi A.,
RA Weinston J.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Weinston S., Harvey G., Mary S., Smith T.,
RA Gibbs R.A., Wein
 Query Match
Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: 1
-!- SIMILARITY: 1
EMBL; AE003676; 1
                                                                                                                                SMART; SM00020; Tryp_SPC; 1.
pROSITE; PS00134; TRYPSIN_HIS;
pROSITE; PS00135; TRYPSIN_SER;
                                                                                                                                                                     Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPc; 1.
                                                                                                                                                                                                                                                            HSSP; P20160; 1A7S.
FlyBase; FBgn0037515; CG3066.
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. Ryu J.H., Lee W.J.;
                                                                                               Hydrolase;
SEQUENCE
                                                                                                                                                                                                                       InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Trypsin.
                                                                                                                                                                                                                                                                                                                                                                           Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20196006; PubMed=10731132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                "Molecular cloning of a
                                                                                                                                                                                                                                                                                                     AF233093;
 Similarity
8; Conser
                                                                                             Serine
391 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Neoptera; Endopterygota; Diptera; Brachycera; Musc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              melanogaster (Fruit fly).
 32.4%;
ilarity 40.0%;
Conservative
                                                                                               ΑĄ;
                                                                                                                                                                                                                                                                                                                     TO SERINE PROTEASES, TRYPSIN FAMILY. TO CHYMOTRYPSIN SERINE PROTEASE FAMILY (S1) AAF54143.1; -.
                                                                                                                                                                                                                                                                                                     AAF43410.1; -.
                                                                                           protease.
                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila
                                                                                               MW;
Score 47; DB Pred. No. 45; S; Mismatches
                                                                                               3E1416F12EDF89F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                serine
             DB
45;
                                                                                                                                                                                                                                                                                                                                                                                                                proteinase
                                      5
7;
                                      Length 391;
                                                                                                                                                                                                                                                                                                                                                                                                                  homologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Muscomorpha;
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Gaps
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RESULT
Q9YMI5
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                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
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045247;
01-JUN-1998
01-MAY-2000
01-MAR-2001
                                                                                                                                                                                                            01-MAY-1999
01-MAY-1999
01-MAY-1999
                                                                                                                                                                                                                                      Q9YMI5
                                              Kuzio J., Pearson M.N.,
Slavicek J., Rohrmann G.
Submitted (AUG-1998) to
                                                                                                                 MEDLINE=99124785; PubMed=9887315;
Kuzio J., Pearson M.N., Harwood S.H.,
Stavicek J.M., Rohrmann G.F.;
                                                                                                                                                                                                                                                                                                                                                                          investigating biology ";
Science 282:2012-2018 (1998).
EMBL; 281468; CABO3875 2; -.
SEQUENCE 1002 AA; 109008 MW;
EMBL; AF081810; AAC70329
                                                                                        "Sequence and analysis of Lymantria dispar."; Virology 253:17-34(1999).
                                                                                                                                                                                Lymantria dispar multicapsid
Viruses; dsDNA viruses, no RN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
                    Kuzio J.;
                                                                                                                                     SEQUENCE FROM N.A. MEDLINE=99124785;
                                                                                                                                                                          Nucleopolyhedrovirus
                                                                                                                                                                                                    LDORF-143 PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (NOV-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Smye R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Caenorhabditis elegans
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                             SEQUENCE FROM N.A.
                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                NCBI_TaxID=10449;
                                                                                                                                                                                                                                                                                                                                                                                                                       none;
                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=99069613; PubMed=9851916.
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                            170 KGLGYHKDQSSVSRKLRLSESSPG--FDQSEC
                                                                                                                                                                                                                                                                                                                                                                                                              'Genome sequence of the nematode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  318 NIHLISSQLCVGGEFYRDSC
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RNA stage; Baculoviridae;
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                                               EMBL/GenBank/DDBJ
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3; Mismatches
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22177 MW;

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DE H'
GN A
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RX MEDLINE-20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
RA Cronin L.A., Shen M., Vanaken S.E., Umayam L., Tallon L.J., Gill J.E.,
RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
RA Salzberg S.L., Fraser C.M., Venter J.C.;
RA Salzberg S.L., Fraser C.M., Venter J.C.;
RI Nature 402:761-768(1999).
DR EMBL, AC018721, AAPI8734.1; -.
DR EMBL, AC018721, AAPI8734.1; -.
DR InterPro; IPRO0102; HLH_dim.
DR SMART; SM00353; H.H.; 1.

RW Hydothetical brotein.
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Matches 9
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01-AUG-1998 ('

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HYPOTHETICAL

AQ_1392;
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Best Local Similarity 38.3
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MEDLINE=99225673; PubMed=10207155;
Wang M.L., Belmonte S., Kim U., Dolan M., Morris J.W., God
"A cluster of ABA-regulated genes on Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ol-NOV-1999 (TrEMBLrel. 12, Created)
Ol-NOV-1999 (TrEMBLrel. 12, Last sequence update)
Ol-NOV-1999 (TrEMBLrel. 17, Last sequence update)
Ol-UN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 28 4 KDA PROTEIN.
TOTMO7.8 OR AT2640200.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                10 SLAFSEISVGAEFNKDDC
                                                                                                                                                                                          Local Similarity 50.0 nes 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                       NLGFSSSSFGGNFPADDC 53
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      (TrEMBLrel. 07, Created)
(TrEMBLrel. 07, Last sequence update)
(TrEMBLrel. 13, Last annotation updat.)
L 33.2 KDA PROTEIN.
                                                                            PRELIMINARY;
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Pred. No.
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Nismatches 8
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                                                                                        Nature 392:353-358(1998).
EMBL; AE000738; AAC07368.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 292 AA; 33244 MW; 38AB3FD436D35FEB CRC64;
                                                                                                                                            Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R., Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
"The complete genome of the hyperthermophilic bacterium Aquifex
261 LKYELDFRLAFSAITLG
                                                                                                                                                                                                                                                 Aquifex aeolicus.
Bacteria; Aquificales; Aquificaceae; Aquifex.
NCBI_TaxID=63363;
                                                                                                                                                                                                      MEDLINE=98196666; PubMed=9537320;
                                                                                                                                                                                                                            STRAIN=VF5
                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
            3 LGYHLDVSLAFSEISVG
                                                10;
                                         Similarity 58.8
10; Conservative
                                                     31.7%;
58.8%;
 277
                      19
                                                   Score 46; DB
Pred. No. 47;
                                      Mismatches
                                                             2;
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Search completed: January Job time: 451 sec 6, 2002, 09:10:38

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                Score
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Gapop 10.0 , Gapext 0.
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Copyright (c) 1993 - 2000 Compugen Ltd
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Human C9 protein f
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544	516	484	484	484	305	298	148	117	77	75	74	58	591	434	1070	567	320	320	309	306	306	295	282	282	271	213	168	154	90		82	330	1547
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AAG46682	AAG46683	AAW99455	AAW02615	AAR97734	AAG82721	AAG91621	AAW56138	AAW51102	AAG75197	AAG46703	AAG46704	AAG46705	AAR74802	AAG82564	AAB11124	AAW20055	AAG40088	AAG13662	AAG31285	AAG40089	AAG13663	AAG31286	AAG40090	AAG13664	AAG31287	AAY27646	AAG38110	AAG38111	AAB41682	AAG74079	AAB54363	AAG62569	AAG38526
Arabidopsis thalia	Arabidopsis thalia	Maize adenylosucci	Maize adenylosucci	Maize adenylosucci		C glutamicum prote	reading			Arabidopsis thalia	Arabidopsis thalia	thal	Saccharomyces sp.	S. epidermidis ope	₽.	Prolyl-tRNA synthe	Arabidopsis thalia	Arabidopsis thalia		thal		Arabidopsis thalia	Arabidopsis thalia		tha	Human secreted pro	Arabidopsis thalia	Arabidopsis thalia	Human ORFX ORF1446	Human colon cancer	Human pancreatic c	Follicular conjunc	Arabidopsis thalia

ALIGNMENTS

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RESULT
AAY27328
CD59 mediated complement; human; Cd59 protein; C9 protein; mimetic; tumour therapy; complement-mediated inflammation; immune disorder; immunovasculitis; rheumatoid arthritis; scleroderma; C5b-9 complex.
       Compounds modulating CD59 mediated complement activity, for treatment of, e.g. immunovasculitis
                                        WPI; 1999-527301/44.
                                                             Sims
                                                                                                                09-FEB-1998;
                                                                                                                                     09-FEB-1999;
                                                                                                                                                           12-AUG-1999.
                                                                                                                                                                               WO9940115-A2
                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                  Human C9 protein fragment (residues 359-384).
                                                                                                                                                                                                                                                                                        05-NOV-1999
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                                                                               (BLOO-) BLOOD CENT RES FOUND INC.
(OKLA-) OKLAHOMA MEDICAL RES FOUND
                                                                                                                                                                                                                                                                                      (first entry)
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Arabidopsis thalia

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RESULT AAY27324 AD AAY2
XX AAY2
XX AAY2
XX AAY2
XX DE Huma
XX CD59
KW Lumc
KW Immu
XX Home
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to compounds modulating CD59 mediated complement CC activity. It provides (1) molecules structurally mimicking human CD59 cC amino acid residues 42-88 (region which serves as binding site for CD59 cC inhibit the formation of the human C5b9 occupies. These mimetics cC specifically bind to amino acid residues 359-384 of human C9. (1i) cC in a spatial orientation which can promote the formation of the C5b-9 cmplex. CD59 cmplex. CD59 cmplex. CD59 cmplex. CD59 cmplex. CD59 cmplex assembly. This is especially useful in cC immune disorders and diseases such as immunovasculitis, rheumatoid cC c5b-9 complex assembly. This is useful in pattents in need of suppression of complement-mediated inflammation, e.g. crarthritis, scleroderma. Compounds that mimic C9 can be used to promote complex assembly. This is useful in pattents in need of complement composition can be administered as an adjunct to tumour vy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local :
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The invention relates to compounds modulating CD59 mediated complement activity. It provides (1) molecules structurally mimicking human CD59 amino acid residues 42-58 (region which serves as binding site for CD59 interactions) when they are in a spatial orientation which can inhibit the formation of the human C55-9 complex. These mimetics specifically bind to amino acid residues 359-384 of human C9. (ii)
                                                                                                                                                                                                        Disclosure;
                                                                                                                                                                                                                                                           Compounds modulating CD59 mediated complement activity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                           (OKLA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W09940115-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CD59 mediated complement; human; Cd59 protein; C9 tumour therapy; complement-mediated inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tumour therapy; coimmunovasculitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human C9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY27324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY27324 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KCLGYHLDVSLAFSEISVGAEFNKDDC 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                  1999-527301/44.
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                                                                                                                                                                                                                                                                                                                                                                                                                              BLOOD CENT RES FOUND OKLAHOMA MEDICAL RES
                                                                                                                                                                                                                                                   of, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein fragment (residues 334-415).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2
                                                                                                                                                                                                  Fig 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0020393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA;
                                                                                                                                                                                                                                                immunovasculitis
                                                                                                                                                                                          75pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptide;
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                                                                                                                                                                                             English.
                                                                                                                                                                                                                                                                                                                                                                                                                              FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 145; DB 20;
Pred. No. 3.4e-17;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ΑA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lammation; immune disorder; scleroderma; C5b-9 complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C9 protein, mimetic;
on; immune disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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Amino acid residues 359-384 of human complement C9 are critical for binding CD59 to C9, resulting in inhibition of C5b-9 complex assembly. Peptides that mimic this human C9-derived peptide sequence, and antibodies raised against such peptides, can be used to modulate binding of CD59 to C9. The peptides bind to endogenous CD59 to prevent the CD59 from inhibiting assembly of the C5b-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local ;
                                                                                             Disclosure; Page 33-35; 51pp; English.
                                                                                                                             Modulating binding of CD59 to C9 complement component that mimics or binds the C9-specific motif, used to activate complement in tumour therapy or to treat complement mediated
                                                                                                                                                                                                                                    Sims
                                                                                                                                                                                            WPI; 1997-289058/26.
N-PSDB; AAT68886.
                                                                                                                                                                                                                                                           (OKLA-)
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                                                                                                                                                                                                                                                                                                                                                                                    Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                        Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antibody; inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complement C9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human complement C9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW18310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW18310 standard; Protein; 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     molecules structurally mimicking C9 amino acids 359-384 when they are in a spatial orientation which can promote the formation of the C5b-9 complex. Compounds that mimic CD59 can be used to increase CD59 patients in need of suppression of complement-mediated inflammation, e.g. inmune disorders and diseases such as immunovasculitis, rheumatoid arthritis, scleroderma. Compounds that mimic C9 can be used to promote activation. The composition can be administered as an adjunct to tumour therapy. The present sequence represents a human C9 protein fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25 rclgyhldvslafseisvgaefnkddc 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KCLGYHLDVSLAFSEISVGAEFNKDDC
                                                                                                                                                                                                                                                    OKLAHOMA MEDICAL RES FOUND
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                                                                                                                                                                                                                                                                                                        96WO-US17940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CD59;
                                                                                                                                                                                                                                                                                                                                                                                  /label= CD59_binding_site
/note= "Claim 1 (amino ac
381..406
                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers 356..437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C5b9 complex; tumour; therapy; contraceptive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97.9%;
96.3%;
                                                                                                                                                                                                                                                                                                                                                                                        1 (amino acids 359-384)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 142; DB 20;
Pred. No. 4.2e-16;
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                                                                                                                                                          uses
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complement-mediated

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                 cc activity. It provides (i) molecules structurally mimicking human CD59 camino acid residues 42-58 (region which serves as binding site for CD59 cc -09 interactions) when they are in a spatial orientation which can cc inhibit the formation of the human C5b-9 complex. These mimetics specifically bind to amino acid residues 359-384 of human C9. (ii) complexity bind to amino acid residues 359-384 of human C9. (ii) complexity bind to amino acid residues 359-384 of human C9. (ii) complexity bind to amino acid residues 359-384 when they are complex. Compounds that mimic C9 amino acids 359-384 when they are cc in a spatial orientation which can promote the formation of the C5b-9 cc inhibition of C5b-9 complex assembly. This is especially useful in C9 atients in need of suppression of complement-mediated inflammation, e.g. cimmune disorders and diseases such as immunovasculitis, rheumatoid carthritis, scleroderma. Compounds that mimic C9 can be used to promote c5b-9 complex assembly. This is useful in patients in need of complement activation. The composition can be administered as an adjunct to tumour composition can be administered as an adjunct to tumour composition can be administered as an adjunct to tumour composition can be administered as an adjunct to tumour composition can be administered as an adjunct to tumour composition can be administered as an adjunct to tumour composition can be administered as an adjunct to tumour composition can be administered as an adjunct to tumour composition can be administered as an adjunct to tumour composition can be administered as an adjunct to tumour composition can be administered as an adjunct to tumour composition can be administered as an adjunct to tumour composition can be administered as an adjunct to tumour composition can be administered as an adjunct to tumour composition can be administered as an adjunct to tumour composition can be administered as an adjunct to tumour composition can be administered as an adjunct to tumour composition can be administered as an
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Best Local :
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(OKLA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CD59 mediated complement; human; Cd59 protein; C9 protein; mimetic; tumour therapy; complement-mediated inflammation; immune disorder; immunovasculitis; rheumatoid arthritis; scleroderma; C5b-9 complex;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Compounds modulating CD59 mediated treatment of, e.g. immunovasculitis
Sequence
                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to compounds modulating CD59 mediated complement
                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 10; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-527301/44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sims PJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rabbit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytolysis
86
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AL RES
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Pred. No. 4.5e-15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement activity, for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18;
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RESULT
AAW18311
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                          Matches
                                     Query Match
Best Local
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                                                                                                         A polypeptide (AAW18311) comprises rabbit complement C9. Chimeric proteins were constructed in which the segment of C9 corresponding to the putative CD59 binding site were interchanged between rabbit and human C9 (see also AAW18310). These were tested for haemolytic activity and for sensitivity to inhibition by membrane CD59. Substn. of human C9 residues 334-415 into rabbit C9 resulted in a protein that was indistinguishable from human C9 in its sensitivity to inhibition by CD59. When this same segment of human C9 was replaced by the corresponding rabbit sequence (aa339-424), the chimera was indistinguishable from rabbit C9 and was virtually unaffected by the presence of membrane CD59.
                                                                                                                                                                                                                                                                                           Modulating binding of CD59 to C9 complement component that mimics or binds the C9-specific motif, used to activate complement in tumour therapy or to treat complement mediated
                                                                                                                                                                                                                                                                                                                                                 N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                     Sims
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antibody; inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complement C9; CD59; C5b9 complex; tumour; therapy; contraceptive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-AUG-1997
                                                                                    Sequence
                                                                                                                                                                                                                                                             Disclosure; Page 36-38; 51pp; English
                                                                                                                                                                                                                                                                                     inflammation
                                                                                                                                                                                                                                                                                                                                                            WPI; 1997-289058/26
                                                                                                                                                                                                                                                                                                                                                                                                                                     15-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-NOV-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9717987-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryctolagus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rabbit complement C9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW18311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW18311 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                           (OKLA-) OKLAHOMA MEDICAL RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25 kclgfdldlslnipgksaglsltgqanknnc 55
 1 KCLGYHLDVSLAF----SEISVGAEFNKDDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 KCLGYHLDVSLAF----SEISVGAEFNKDDC
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                         l Similarity
12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l Similarity
12; Conserv
                                                                                      561
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                          Conservative
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                                                                                      AA;
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38.7%;
                                   39.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              561
                          8
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                                     Score 57; I
                                                                                                                                                                                                                                                                                                                                                                                                            FOUND
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Pred. No. 0.063;
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                          Mismatches
  27
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                                DB 1
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                                                  18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7;
                                                  Length 561;
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                          Indels
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kclgfdldlslnipgksaglsltgqanknnc 418

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CC detoxifying fumonisin or a structurally related mycotoxin present in CC during processing, or to application to a plant or to harvested grain or a structurally related mycotoxin present in CC during processing, or to processed grain that is to be used as animal CC into microorganisms that multiply on plants to the present CC into microorganisms that multiply on plants to deliver enzymes to CC introduced via a vector into a microbial host and the transformed host CC introduced via a vector into a microbial host and the transformed host CC invention are fermented in a bacterial host and the resulting the CC is supplied to the environment, plants or animals for reducing the CC invention are fermented in a bacterial host and the resulting bacteria CC can be used alone or in combination to engineer microbes or other CC crossisms to metabolise fumonisin and resist its toxic effects.
      Best Local Similarity
                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
AAY72637
                                                                    Sequence
                                                                             The present protein sequence is p-glycoprotein, a fumonisin degradative enzyme from Exophiala spinifera.
                                                                                                                                                                                                                                                                                                             aldehyde dehydrogenase, permease and p-glycoprotein. A fumonisin esterase enzyme with at least one fumonisin degradative enzyme is useful for
                                                                                                                                                                                                                                                                                                                                          The patent discloses novel polynucleotides encoding Exophiala spinifera fumonisin degradative or transport enzymes such as flavin monooxygenase,
                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1c; Page 77-82; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                            Novel polynucleotides encoding Exophiala degradative or transport enzyme which is useful for detoxifying fumonisin or structurally related mycotoxin during processing of grain for human or animal food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAD02694, AAD02695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PION-) PIONEER HI-BRED INT INC. (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Exophiala spinifera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    aldehyde dehydrogenase; permease; p-glycoprotein; fumonisin detoxification; mycotoxin; animal feed; human feed; silage; transgenic plant; transgenic animal; microbial spray.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Exophiala spinifera p-glycoprotein, a fumonisin degradative enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fumonisin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-MAY-2001
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                                                                    1263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               degradative enzyme; transport enzyme; flavin monooxygenase;
                                                                 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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    34.5%;
42.1%;
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   Score
Pred.
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 50;
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DВ
25;
            22;
           Length 1263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Crasta
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by a TGA codon in the CDNA (see AAZ34468). Polymorphisms in the CDNA (se
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  Sequence
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                                                                                                                                                                                                                                                                                                                                  The present sequence represents a mouse 15 kDa selenoprotein that is differentially expressed in cancer cells, such as cancer cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated selenoprotein polypeptides, used to detecting susceptibility to or treating cancers
                                                                                                                                                                                                                                                                                                            It includes a selenocysteine residue at position 93 that is encoded
                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gladyshev VN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prostate cancer; diagnosis; polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse 15 kDa selenoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Selenoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-2000
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:| |:| |:| |::|
922 rcfgfhlsqsmeflaialg 940
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  162
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AA;
                                                                                                                                                                                                                                                                                                                                                                                                                   60;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wootton JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-0080850
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93
                                                                                                                                                                                                                                                                                                                                                                                                          67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "selenocysteine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hatfield DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jeang
                                                                                                                                                                                                                                                                                                                                                                                                                                                       to develop products for rs e.g. prostate cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ×.
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Query Match Best Local Similarity

Conservative

5

Mismatches

Length Indels

Gaps

1;

30.7%; 42.3%;

Score 44.5; Pred. No. 16;

DВ

21; 9;

162;

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AAU02929
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     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          converting e
                                                                                                                                                                                                                      polypeptide receptor 2. The polypeptides and their associated nucleic acids are useful for identification of variant sequences and detection candidate compounds capable of binding the molecules. The sequences of the invention can be used in the treatment and diagnosis of various disorders including cardiovascular diseases such as arteriosclerosis, myocardial infarction and coronary arterial thrombosis, renal diseases such as diabetic nephropathy, muscular diseases such as hypertrophy, lamune disorders such as immune complex nephritis, multiple sclerosis, and the properties of the property of the pro
                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence represents an angiotensin converting enzyme splice variant (ACEV) polypeptide. The polypeptides of the invention include variants of granulocyte colony stimulating factor receptor, glucagon, interleukin 6, platelet-derived endothelial cell growth factor, cyclin-dependent kinase inhibitor 10, cellular tumour antigen P53, and vasoactive intestinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel alternative splicing variants e.g. variant of angiotensin converting enzyme (ACEV), useful in identifying candidate compounds capable of binding to the variant and to detect anti-variant antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer; myocardial infarction; coronary arterial thrombosis; renal disease; diabetic nephropathy; muscular disease; immune disorder; sarcoidosis; multiple sclerosis; immune complex nephritis; deep vein thrombosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Angiotensin converting enzyme splice variant; ACEV; interleukin b; granulocyte colony stimulating factor receptor; glucagon; hypertrophy; platelet-derived endothelial cell growth factor; cardiovascular disease; cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1C;
                                                                                                                                                                         cancer, sarcoidosis, nonarcoidotic pulmonary granulomatous diseases as asbestosis and vascular pathologies involving an endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nonarcoidotic pulmonary granulomatous vascular disorder; asbestosis.
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                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4;
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10-DEC-1999;
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                                                                                                                                                                                                                                                               infections and in diagnostic assays for detecting disease associated with microbial infections. The polypeptides and polynucleotides are also useful as microbial vaccines. The polypeptides are also used to
                                                                                                                                                                                                                                                                                              The present sequence represents a tktA polypeptide from Staphylococcus aureus. The polypeptides and polypucleotides are useful for treatment of microbial infections, identifying agonists and antagonists for treating microbial infections and conditions associated with such
        Arabidopsis thaliana
                                                                       AAG38528
                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 4; 41pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tktA; microbial infection; microbial vaccine;
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                              18-OCT-2000
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Similarity 36.4%;
8; Conservative
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Pred. No. 1.1e+02;
6; Mismatches 8;
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         fragment
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         SEQ ID NO: 47543
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9905-0139460 9905-0139461 9905-0139462 9905-0139463 9905-0139750 9905-0139753 9905-0139753 9905-0139817 9905-0139819 9905-0139813	99US-0139452. 99US-0139453. 99US-0139492. 99US-0139454. 99US-0139456. 99US-0139457. 99US-0139458.	99US-0135124. 99US-013523. 99US-0135639. 99US-0136021. 99US-0136392. 99US-0137722. 99US-0137728. 99US-0137724. 99US-0137724. 99US-0137724. 99US-0138647. 99US-0138847. 99US-0138847.	99US-0131449 99US-0132048 99US-0132048 99US-0132487 99US-0132485 99US-0132486 99US-0132486 99US-0132486 99US-0132486 99US-0134218 99US-0134218 99US-0134218 99US-0134218 99US-0134219 99US-0134219 99US-0134219	2000EP-0301439. 99US-0121825. 99US-0123548. 99US-0125788. 99US-0126764. 99US-0126764. 99US-0127462. 99US-0127462. 99US-0128234. 99US-0128034. 99US-0130077. 99US-0130077. 99US-0130077.	uence.
					mapping; gene expression
					control;
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RESULT 11
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AC AAG385
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KW termin
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Best Local Similarity 47.6%;
Matches 10; Conservative
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                                                       Protein identification; signal transduction pathway; metabolic hybridisation assay; genetic mapping; gene expression control; termination sequence.
  EP1033405-A2.
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                                                                                                              Arabidopsis thaliana protein fragment SEQ ID NO: 47542.
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RESULT 12
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                                                                                                 Arabidopsis thaliana
                                                                                                                        Protein identification; signal transduction pathway; metabolic hybridisation assay; genetic mapping; gene expression control; termination sequence.
                                                                                                                                                           Arabidopsis thaliana protein fragment SEQ ID NO: 47541.
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99US-0123180
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99US-0158029

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99US-0158232

99US-0159294

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47
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3; Mismatches
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PR 02-JUL-1999; 99US-0142055
PR 08-JUL-1999; 99US-0142390.
PR 109-JUL-1999; 99US-0142390.
PR 12-JUL-1999; 99US-0143524.
PR 11-JUL-1999; 99US-0144085.
PR 15-JUL-1999; 99US-0144331.
PR 119-JUL-1999; 99US-0144332.
PR 119-JUL-1999; 99US-0144333.
PR 119-JUL-1999; 99US-0144333.
PR 119-JUL-1999; 99US-0144333.
PR 12-JUL-1999; 99US-0144333.
PR 12-JUL-1999; 99US-0144333.
PR 22-JUL-1999; 99US-0144333.
PR 22-JUL-1999; 99US-0144662.
PR 22-JUL-1999; 99US-0144662.
PR 22-JUL-1999; 99US-0144662.
PR 22-JUL-1999; 99US-014508.
PR 22-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0146388.
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         Disclosure; Page 23-25;
                                 New adenovirus for the prevention and treatment of Ad infection
                                                                                                                                               (ITON/) ITO N.
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                                                                                                                                                                                                                                                                                                JP2001095583-A.
                                                                                                                                                                                                                                                                                                                                   Mastadenovirus
                                                                                                                                                                                                                                                                                                                                                             Follicular conjunctivitis; antiserum;
                                                                                                                                                                                                                                                                                                                                                                                       Follicular conjunctivitis related adenoviral protein SEQ ID NO: 10.
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ARB54466. The human pancreatic cancer antigens, given in ARB54008 to neuroprotective, nootropic, immunomodulatory, relaxant, contraceptive, gynaecological, cardiant and antiinflammatory activities, and can be used preventing, treating, or ameliorating a medical condition or in assays subject. Binding partners to the proteins and the activity to one in a proteins can be identified. The pancreatic cancer antigens can be used to detect, treat or prevent pancreatic disorders, especially cancer. Agonists and antagonists to the antigens can be screened for The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Matches 11
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                                                                                                                                                                                                                                                                                                  AAC98773 to AAC99231 encode the human pancreatic cancer associated
                                                                                                                                                                                                                                                                                                                                                                    Claim 11; Page 1271; 1379pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-579444/54.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB54363 standard;
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ion; diagnosis; identification; cytostatic;
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                                                                                                                            AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pancreatic cancer antigen polynucleotides can be used to design nucleic acid hybridisation probes that can be used in chromosome mapping, linkage analysis, tissue identification and/or typing and a variety of forensic and diagnostic methods. The proteins can be used to generate antibodies which are used to purify, detect and target the polypeptides, including both in vivo and in vitro diagnostic and therapeutic methods. The proteins can be used to treat or prevent neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal or proliferative disorders. AAC99232 to AAC99240 and AAB54467 represent
                         inactive proteins or to supplement the patients own production of P., Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnos
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -
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03-NOV-1999;
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N.B. Pages 666 to 682 and page 7053 of the missing at time of publication, meaning no SEQ ID NO:1027 to 1052, 7921 and 7922.
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US-08-559-492-5
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                                                                                                                                                                                                                     Sequence 5, Application US/08559492 Patent No. 5843884
                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Sims, Peter J.
TITLE OF INVENTION: C9 Complement Inhibitor
NUMBER OF SEQUENCES: 16
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ZIP: 1036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
COMPUTER: PC-DOS/MS-DOS
COMPUTER: PC-DOS/MS-DOS
         ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,288B
FILING DATE: January 5, 1995
CLASSIFICATION: 435
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                                                                                                                                             CORRESPONDENCE ADDRESS:
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APPLICANT: Jessell,
TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
                                                                                 ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center, 1201 West Peachtree
STREET: Street
CITY: Atlanta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 40
TELECOMMUNICATION INFORMATION:
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STREET: New York
CITY: New York
"MATE: New York
                                                                                                                                  ADDRESSEE:
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NAME: White, John P.
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CORRESPONDENCE ADDRESS:
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TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: White, John P.
REGISTRATION NUMBER: 28,678
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STREET: 1185 Avenue of the Americas
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96.3%;
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Pred. No. 2.1e-15;
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US-08-559-492-4
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Patent No. 5843884
GENERAL INFORMATION:
                                                                                         TELEFAX: 404-873-8795
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local Similarity 96.3%;
                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 86 amino acids
MOLECULE TYPE:
                                                                                                                                                 CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,2
REFERENCE/DOCKET NUMBER:
                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 404-873-8794
                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Sims, Peter J.
TITLE OF INVENTION: C9 Complement Inhibitor
NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
             TOPOLOGY:
                          STRANDEDNESS:
                                                TYPE:
                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 15-NOV
                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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FILING DATE: 15-NOV-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 30309-3450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               380 RCLGYHLDVSLAFSEISVGAEFNKDDC 406
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STREET: Street
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TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OM
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                                          amino acid
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Pred. No. 2.1e-15;
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Matches Query Match

Local

COUNTRY:

STATE:

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                                                                                                         Sequence 3, Application US/08729345 Patent No. 5849999
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                                                                                            GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION UNMBER: 31,284
REFERENCE/DOCKET NUMBER: OM
TELECOMMUNICATION INFORMATION:
             APPLICANT: Neve, Rachael L.
APPLICANT: Berger-Sweeney, Joanne
TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMAL
TITLE OF INVENTION: EXPRESSING FLAG-APP-C100 FUSION PROTEIN
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino a STRANDEDNESS:
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FILING DATE: 15-NOV-1995
CLASSIFICATION: 424
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N: C9 Complement Inhibitor
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38.7%;
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38.7%;
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Pred. No. 0.025;
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APPLICATION NUMBER: US/08/565
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Timian, Susan J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 176/
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                      CITY: Roches
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                        APPLICANT: Bavoil, Patrik M.
APPLICANT: Hsia, Ru-ching
TITLE OF INVENTION: BACTERIOPHAGE OF CHLAMYDIA PSITTACI
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS LENGTH: 117 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T
REGISTRATION NUMBER: 30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 800 PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ Version 2.0 CURRENT APPLICATION DATA:
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OPERATING SYSTEM:
SOFTWARE: FastSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/0: FILING DATE: 16-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                           STREET:
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TELEFAX: 617-542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
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                                                                                                                        US/08/565,386
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                     176/60040
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Pred. No. 11;
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; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (288)
US-09-347-798-12
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US-08-361-611-4
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APPLICANT: Cahoon, Rebecca E.
APPLICANT: Hitz, William D.
APPLICANT: Rafalski, Antoni
TITLE OF INVENTION: Ornithine Biosynthesis Enzymes
FILE REFERENCE: BB-1174-B
CURRENT APPLICATION UNMBER: US/09/347,798
CURRENT FILING DATE: 1999-07-02
EARLIER APPLICATION UNMBER: 60/093,209
EARLLER ETLING DATE: 1114 17, 1998
                                                                                                                                                                Sequence 4, Application US/08361611
Patent No. 5519125
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 12
LENGTH: 359
TYPE: PRT
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Best Local
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                             NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 18
SOFTWARE: Microsoft Office 97
                                                                             APPLICANT: Potter, Sharon L
APPLICANT: Ward, Eric R
TITLE OF INVENTION: Plant Adenylosuccinate Synthetase and
TITLE OF INVENTION: DNA Coding Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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TELEFAX: 716-263-1600
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 148 amino acids
COUNTRY:
                                                                                                                                                                                                                                                  267 MSVSRSFNQITVDGDTSTNDC 287
                                                                                                                                                                                                                                                                                                                Local Similarity es 7; Conserv
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mes 7; Conserv
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STRANDEDNESS: not
TOPOLOGY: linear
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             Hawthorne
NY
USA
                                                                                                                                                                                                                                                                                                           Conservative
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33.3%;
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36.8%;
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Pred. No.
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Pred. No.
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48;
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US-08-565-655-4
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              TELEFAX: (919) 541-86
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/08565655
Patent No. 5688939
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Best Local
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                                         ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8614
                                                                                                                        CLASSIFICATION: 210
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/361,611
FILING DATE: 12-DEC-1994
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                       CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (919) 541-8614
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Ciba Patent Department
STREET: 540 White Plains Rd., POB
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Potter, Sharon L
APPLICANT: Ward, Eric R
TITLE OF INVENTION: Plant Adenylosuccinate Synthetase and
TITLE OF INVENTION: DNA Coding Therefor
                                                                                                                                                                                                                                               COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                          SOFTWARE:
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NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30B CURRENT APPLICATION DATA:
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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SYSTEM: PC-DOS/MS-DOS
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45.0%;
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Pred. No. 70;
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Query Match
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                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear; MOLECULE TYPE: protein US-08-946-967-4
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                                                                                                      RESULT 12
US-09-231-529-3
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                                                                       Sequence 3, Applica Patent No. 6096308
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Best Local Similarity
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                                          GENERAL INFORMATION:
APPLICANT: Lal, P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (919) 541-8614
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 4:
            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: ELMET, James Scott
REGISTRATION UNMBER: 36,129
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.30B CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Plant Adenylosuccinate Synthetase and TITLE OF INVENTION: DNA Coding Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Potter, Share APPLICANT: Ward, Eric R
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CORRESPONDENCE ADDRESS:
APPLICANT:
                                                                                                                                                                391 LDVLSGLSEIKVGVSYTQTD 410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Hawthorne STATE: NY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
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                                                                                       Application US/09231529
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       Lal, Preeti
Hillman, Jennifer L.
Bandman, Olga
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45.0%;
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Pred. No. 70;
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Pred. No.
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                                                                                                                                                                                                                                                                         Sequence 3, Application US/08977816 Patent No. 6194186
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Best Local S
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                                                                                                                                                                                              APPLICANT:
APPLICANT:
         COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc
STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IMMEDIATE SOURCE:
LIBRARY: KIDNN
CLONE: 353694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: HUMAN PROTEIN KINASE AND KINASE INHIBITORS
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
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                                                                                                                                             LILLE OF INVENTION: HUMAN PROTEIN KINASE AND KINASE INHIBITORS NUMBER OF SEQUENCES: 9
                                                                       STREET: 3174 POI
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/231,529 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM CONTROL OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: sir
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COMPUTER:
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Similarity 38.5%;
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Hallman, Jennifer L.
Bandman, Olga
Corley, Neil C.
Shah, Purvi
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 IBM Compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               650-855-0555
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Pred. No. 59;
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RESULT 14
US-08-262-220-6
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Best Local Similarity
Watches 10; Conserve
                             INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/262
FILING DATE: 20-JUN-1994
CLASSIFEICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVER P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: BERG,
TELECOMMUNICATION INFORMATION:
TELECHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Application US/08262220 Patent No. 6054296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELECHONE: 650-855-0555
                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                  TELLEFAX: 200
TELLEFAX: 248633
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                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: BARBOUR ALÂN G.
TITLE OF INVENTION: NEW 66 KDA ANTIGEN FROM BORRELIA
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
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STRANDEDNESS: si-
TOPOLOGY: 1

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LENGTH: 4619 amino acids
                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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LENGTH: 365 amino acid
                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 SEVENTH STREET, N.W.
CITY: WASHINGTON
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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LIBRARY: NIL
NE: 353694
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KCLG-----YHLDVSLAFSEIS 17
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Pred. No. 59;
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Best Local Similarity
Thes 9; Conserve
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US-08-471-733-6
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Best Local Similarity 45.0
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                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: BERGST
APPLICANT: BARBOU
                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 619 amino acid
                                                                                                                                                                                                                                     NAME: COOPER, IVER P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: BE
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/21
FILING DATE: 20-JUN-1994
ATTORNEY/AGENT INFORMATION:
372 ELGIAFSTGASIGLAWNKDD 391
                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: BERGSTROM SVEN
APPLICANT: BARBOUR ALAN G.
TITLE OF INVENTION: NEW 66 KDA ANTIGEN FROM BORRELIA
NUMBER OF SEQUENCES: 14
                                                                                                                                                             TYPE:
                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                               TELEPHONE: 202 737-3528
                               8
                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              372 ELGIAFSTGASIGLAWNKDD 391
                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/0 FILING DATE: 06-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: WASHINGTON
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                        DVSLAFSE-ISVGAEFNKDD 26
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419 SEVENTH STREET, N.W.
                                                    Conservative
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45.0%;
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45.0%;
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                                                              Score 41.5;
Pred. No. 1
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Search completed: January Job time: 194 sec

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Maximum Match
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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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S18575
S18575
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F11229
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F1127
S2677
S32677
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P10272
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cofact
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ALIGNMENTS

RESULT A61612

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allatostatin - tobacco hornworm

C;Species: Manduca sexta (tobacco hornworm)

C;Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 11-Jul-1997

C;Accession: A61612
R;Kramer; S.J.; Toschi, A.; Miller, C.A.; Kataoka, H.; Quistad, G.B.; Li, J.P.; Carne Proc. Natl. Acad. Sci. U.S.A. 88, 9458-9462, 1991
A;Title: Identification of an allatostatin from the tobacco hornworm Manduca sexta. A;Reference number: A61612; MUID:92052112
A;Recession: A61612
A;Status: preliminary
                                                                          A:Reference number: PC2214; MUID:9429641
A:Accession: PC2215
A:Molecule type: protein
A:Residues: 1-15 <HUN>
C:Keywords: hydrolase; serine proteinase
                                                                                                                                                                                                                                         fibrinogenolytic proteinase A2 (EC 3.4.21.-) - western diamondback rattlesnake (fragm N;Alternate names: alpha-fibrinogenase A2 C;Species: Crotalis atrox (western diamondback rattlesnake) C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 17-Mar-1999 C;Accession: PC2215 R;Hung, C.C.; Chiou, S.H.
                                                                                                                                                                                                       Biochem. Biophys. Res. Commun. A; Title: Isolation of multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: protein
A; Residues: 1-15 <KRA>
C; Keywords: neuropeptide;
F; 1/Modified site: pyrroli
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pyrrolidone_carboxylic acid (Gln) #status experimental
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26.0%;
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C;Accession: PS0371
R;Rhiel, E.; Stirewalt, V.L.; Gasparich, G.E.; Bryant, D.A.
Gene 112, 123-128, 1992
A;Title: The psaC genes of Synechococcus sp. PCC7002 and Cyanophora paradoxa: cloning an A;Accession: PS0371
A;Accession: PS0371
 A;Cross-references: GB:M86238; NID:g154574; PIDN:AAA27351.1;
                                A; Molecule type: DNA
A; Residues: 1-14 <RHI>
                                                                                                                               hypothetical protein (psaC region) - Synechococcus sp. (fragment)
C;Species: Synechococcus sp.
C;Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: protein
A; Residues: 1-9 <TSO>
C; Keywords: transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Tsolas, O.; Sun, S.C.
Arch. Biochem. Biophys. 167, 525-533, 1975
A;Title: Isolation of a peptide containing a
A;Reference number Al1497; MUID:75145197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transaldolase (EC 2.2.1.2) III - yeast (Pichia jadinii) (fragment) C;Species: Pichia jadinii, Candida utilis C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 30-Sep-1993
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Best Local Similarity 5/...
Best Local Similarity 5/...
Conservative
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A; Accession: H56046
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PID: g552030
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RESULT 8
G4939
T-cell receptor beta chain V-D-J-C region (V beta 4, J beta 2.2) -
C;Species: Homo sapiens (man)
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 30-
C;Accession: G49039
                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: protein
A;Molecule type: protein
A;Residues: 1-16 <LOU>
C;Superfamily: alpha-conotoxin
C;Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic |
F;1-16/Product: alpha-conotoxin EpI #status experimental <MAT>
F;2-8,3-16/Disulfide bonds: #status experimental <MAT>
F;15/Binding site: sulfate (Tyr) (covalent) #status experimental
F;16/Modified site: amidated carboxyl end (Cys) #status experimental
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Best Local Similarity
"~~~hes 3; Conserv:
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c;Species: Conus episcopatus (bishop's cone)
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 13-Aug-1999
C;Accession: A59042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Alpha-conotoxin EpI, a novel sulfated peptide from Conus episcopatus that se A;Reference number: A59042; MUID:98288307
A;Accession: A59042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R; Loughnan, M.; Bond, T.; Atkins, A.;
J. Biol. Chem. 273, 15667-15674, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Experimental source: pancreatic islets C; Superfamily: kexin; subtilisin homology C; Keywords: hydrolase; serine proteinase
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Endocrinology 129, 2263-2265, 1991
A:Title: Identification of a somatostatin-14-generating propeptide converting A;Reference number: A61117; MUID:92007528
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Best Local Similarity 71.4
Matches 5; Conservative
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3; Conserv
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             #sequence_revision 18-Nov-1994 #text_change 30-May-1997
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71.4%;
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Pred. No. 2.2e
1; Mismatches
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Pred. No. 1.6e
3; Mismatches
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Pred. No. 1.3e+03;
1; Mismatches 1
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2.2e+03;
1;
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                                                       human (fragment)
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botulinum neurotoxin type E - Clostridium botulinum (strain Alaska E-43) (fragment) C;species: Clostridium botulinum A;species: Clostridium botulinum (strain Alaska E-43) (fragment) A;Variety: strain Alaska E-43 C;bate: 19-Mar-1997 #sequence_revision 21-Nov-1998 #text_change 21-Nov-1998 C;Accession: 508575 R;Schmidt, J.J.; Sathyamoorthy, V.; DasGupta, B.R. Arch. Biochem. Biophys. 238, 544-548, 1985 A;Ritle: Partial amino acid sequences of botulinum neurotoxins types B and E. A;Reference number: S07128; MUID:85197963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Rosenberg, W.M.; Moss, P.A.; Bell, J.I.

Bur. J. Immunol. 22, 541-549, 1992

A;Title: Variation in human T cell receptor V beta a
A;Reference number: A49039; MUID:92164737

A;Accession: G49039

A;Status: preliminary; not compared with conceptual
A;Molecule type: nucleic acid
A;Mosidus: 1-16 <ROS>
A;Note: sequence extracted from NCBI backbone (NCBIP
C;Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein [imported] - Haloarcula marismortui (fragment) c;Specles: Haloarcula marismortui (fragment) C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 21-Jul-2000 C;Accession: T46794
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T46794
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A;Molecule type: DNA
A;Residus: 1-12 <ARN>
A;Cross-references: EMBL:X55311; NID:g43610;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Nucleotide sequence of four genes encoding A;Reference number: S10731; MUID:90336772 A;Accession: T46794
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F;1-13/Product: botulinum
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Matches 3
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A; Residues: 1-16 <RES>
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                                                            C; Keywords: transferase
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C:Accession: A12872
R:Sun, S.C.: Joris, L.; Tsolas, O. R:Sun, S.C.: Joris, L.; Tsolas, O. R:Sun, S.C.: Joris, L.; Tsolas, O. R:Sun, S.C.: Joris, L.; Tsolas, O. R:Sun, S.C.: Joris, L.; Tsolas, O. R:Sun, S.C.: Joris, L.; Tsolas, O. R:Sun, S.C.: Joris, L.; Tsolas, O. R:Sun, S.C.: Joris, L.; Tsolas, O. R:Sun, S.C.: Joris, L.; Tsolas, O. R:Sun, S.C.: Joris, J.; Tsolas, O. R:Sun, S.C.: Joris, Jori
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             aldehyde dehydrogenase (EC 1.-.-) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                        transaldolase (EC 2.2.1.2) I - yeast (Pichia jadinii) (fragment) C;Species: Pichia jadinii, Candida utilis C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change
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C;Species: Ctenopharyngodon idella (grass carp)
C;Date: 14-Apr.1998 #sequence_revision 24-Apr.1998 #text_change
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A; Title: Characterization of a functional recombinant rat liver aldehyde dehydrogenas
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Pred. No. 2.2e+05;
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Pred. No. 3.1e+03
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Score Pred.

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DB 2; 2.2e+05;

Length

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RESULT 16
S32677
nitrogenase cofactor synthesis protein nifs - Anabaena variabilis (fragment)
N;Contains: L-cysteine sulfurtransferase (EC 2.8.1.-)
C;Species: Anabaena variabilis
C;Accession: S32677
R;Monnerjahn, U.; Boehme, H.
Submitted to the EMBL Data Library, December 1992
A;Description: Cloning and expression in E. coli of the Anabaena.
A;Accession: S32677
A;Accession: S32677
A;Accession: S32677
A;Accession: S32677
A;Cession: S32677
A;Accession: S32677
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FEBS Lett. 317, 53-56, 1993
A;Title: Association of three small GTP-binding proteins with cholinergic synaptic vesi.
A;Reference number: S29485; MUID:93154521
                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: protein A; Residues: 1-14 < VOL>
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A;Molecule type: protein
A;Residues: 1-14 <MAR>
C;Superfamily: decorin; leucine-rich alpha-2-glycoprotein repeat homology; proteoglycan
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change
C;Accession: pr0077
R;Marcum, J.A.; Thompson, M.A.
Biochem. Biophys. Res. Commun. 175, 706-712, 1991
A;Title: The amino-terminal region of a proteochondroitin core p
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Pred. No. 4e+03;
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4e+03;
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PT0272

Ig heavy chain CRD3 region (clone 3-103B) - human (fragment) C.Species: Homo sapiens (man) C.Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_cha C:Accession: PT0272
                                                                                                                                                                                                                                                                                                                                                      A;Reference number: A92504; MUID:85105003
A;Accession: D22595
A;Accession: D22595
A;Accession: D22595
A;Molecule type: protein
A;Molecule type: protein
A;Residues: 1-17 <ARG>
C;Keywords: amidated carboxyl end; hemolysis; venom
F;17/Modified site: amidated carboxyl end (Val) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Bombus pennsylvanicus (American common bumblebee) C;Date: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_chalc;Accession: D22595 C;Accession: D22595 R;Argiolas, A.; Pisano, J.J. J. Biol. Chem. 260, 1437-1444, 1985 A;Title: Bombolitins, a new class of mast cell degranulating A;Reference number: A92504; MUID:85105003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: PA0009
R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
submitted to JIPID, July 1994
A;Description: Separation and characterization of A.
A;Reference number: PA0001
A;Accession: PA0009
A;Molecule type: Protein
A;Residues: 1-15 (KAMD)
A;Besidues: 1-15 (KAMD)
A;Besidues: 1-15 (KAMD)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Experimental source: seed
C;Keywords: seed; storage protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seed storage protein beta-chain 7 - Arabidopsis thaliana (fragment) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 23-Mar-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-15 <MON>
A;Cross-references: EMBL:X69898; NID:q296503;
C;Superfamily: nitrogen fixation protein nifs
C;Keywords: sulfurtransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 42.9
3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                American common bumblebee
                                                                                                                                                                                                                                                                                             20.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20.8%;
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Pred. No. 4.8e
2; Mismatches
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Pred. No.
                                   30-Sep-1993 #text_change
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2;
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4.3e+03;
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                                 16-Aug-1996
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C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0895; PH0895; PH0896
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B
J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experime A; Reference number: PH0891; MUID:92078857
A;Accession: PH0895
A;Accession: PH0895
A;Residues: 1-10 <GOL>
A;Experimental source: myelin basic protein-immunized T-cell; clones 15 and C;Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: A42266
R;Eipper, B.A.; Green, C.B.; Campbell, T.A.; Stoffers, D.A.; Keutmann, H.T.; Mains, R.E.
J. Biol. Chem. 267, 4008-4015, 1992
A;Title: Alternative splicing and endoproteolytic processing generate tissue-specific fd A;Reference number: A42266; MUID:92156145
A;Accession: A42266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N;Alternate names: peptidylglycine alpha-amidating monooxygenase
C;Species: Rattus norvegicus (Norway rat)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 26-May-1995
                                                                                                                                                                                                                                                                                                                                                                                PHO895
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A; Residues: 1-9 < YAM>
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A; Residues: 1-9 <EIP>
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                              δÃ
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Best Local Similarity 75.0
Matches 3; Conservative
                                                                                     Query Match
Best Local
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Best Local
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Title: Preferential utilization of specific immunoglobulin heavy chain div. Reference number: PT0222; MUID:91108337
                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                receptor beta chain V-D-J region - rat (fragment)
                                                                                     Local Similarity
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CASSDSSERL
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50
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Pred. No.
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Pred.
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No.
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2.2e+05;
3;
                                                                                      4.1e+03;
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                                                                    Indels
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S36889
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PH1627
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C;Species: Mycobacterium bovis
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Jan-1995
C;Accession: S36889
R;Ohara, N.; Kimura, M.; Higashi, Y.; Yamada, T.
FEBS Lett. 331, 9-14, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Reference number: PH1580; MUID:9: A;Accession: PH1627
A;Molecule type: DNA
A;Residues: 1-14 <LEV>
A;Experimental source: bone marrow
C;Keywords: immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Residues: 1-11 <MIY>
C; Comment: This is a chimeric er
C; Comment: The parental enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: synthetic
C;Date: 28-May-1999 #sequence_revision 28-May-1999 #text_change 28-May-1999
C;Accession: PC2124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Levinson, D.A.; Campos-Torres, J.; Leder, P. J. Exp. Med. 178, 317-329, 1993
A;Title: Molecular characterization of transgene-induced A;Reference number: PH1580; MUID:93301609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig H chain V-D-J region (clone B-less 120) - mouse (fragment) C;Species: Mus musculus (house mouse) C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_chan C;Accession: PH1627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: PC2124
A; Molecule type: DNA
A; Residues: 1-11 <MIY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Miyazawa, K.; Kawaguchi, S.; Okamoto, A.; Kato, R.; Ogawa, T.; Kuramitsu, S. J. Blochem. 115, 568-577, 1994
A;Title: Construction of aminotransferase chimeras and analysis of their substrate A;Reference number: JX0315; MUID:94334304
                                                                                          A; Title: Isolation and amino acid sequence A; Reference number: S36887; MUID:94009653
C; Keywords: protein biosynthesis; ribosome
                  A; Molecule type: protein A; Residues: 1-15 <OHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Keywords: aminotransferase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aminotransferase chimera DY376 - synthetic (fragment)
                                                        A; Status: preliminary
                                                                          A; Accession: S36889
                                                                                                                                                                                                                                 ribosomal protein S20 - Mycobacterium bovis (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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RESULT 25
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H+transporting ATP synthase (EC 3.6.1.34) gamma chain, mitochondrial - mouse (fragment) C.Speciles: Mus musculus (house mouse) C.Accession: Pr0095
R.Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Morimasa, T.; Tsugita, A. A. PDescription: Proteome analysis of mouse brain.
A.Pescription: Proteome analysis of mouse brain.
A.Reference number: Pr0091
A.Accession: Pr0095
A.Molecule type: Protein
A.Residues: 1-15 <KAWA
A.Experimental source: brain, striatum C.Keywords: hydrolase; mitochondrion
Search completed: April 2, 2002, 09:25:00 Job time: 114 sec
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RESU TAL3 ID AC DT DT DT OS OC OC	Que Bes Mat Qy	RESULT ALLS_M ALLS_M ADD AC OC		
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TANDARD; PRT; 9 AA. 15, Created) 15, Last sequence update) 28, Last annotation update) I (EC 2.2.1.2) (FRAGMENT). Yeast) (Candida utilis). ; Ascomycota; Saccharomycotina; s; Saccharomycetaceae; Pichia.	; Score 28 ; Pred. No 2; Misma	NDARD; PRT; 15 AA 32, Created) 32, Last sequence update) 39, Last annotation updat AS). acco hawkmoth) (Tobacco h ; Arthropoda; Tracheata; a; Endopterygota; Lepidop gidae; Sphinginae; Manduc pubMed-1946359; i. A., Miller C.A., Kataok i. A., Miller C.A., Kataok i. A., Schooley D.A.; an allatostatin from the Sci. U.S.A. 88:9458-9462(NGLY INHIBITS JUVENILE HO ALLATA FROM FIFTH-STADIU LONGS TO THE ALLATOSTATIN 1 PYRROLIDONE CA 11 PYRROLIDONE CA 11008 MW; 1605B77CDEBC83	ALIGNMENTS	FIBA_MELME LE05_BIOGL EFG_THEAO OXYT_OCTVU T2P1_PROVU MM01_RAT FIBA_EQUAS FOR2_MYRGU UYSX_BPT6 VPR_HV1C3 ALYS_MYCPH BOL1_MEGDE ASP2_LACSN CCAP_CARMA UHA2_HUMAN
	; DB 1; . 75; tches 4	RT; 15 AA. ence update) tation update)) (Tobacco hornworm) Tracheata; Hexapoda ota; Lepidoptera; Glu inae; Manduca. 9; C.A., Kataoka H., Qu C.A., Kataoka H., Qu c.A.; Kataoka	ENTS	ZPZEE CO CC FE
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P56675;
15-JUL-1999
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15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Platyprepia virginalis (Ranchman's tiger moth).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Noctuoidea; Arctiidae; Platyprepia.
NCBI_TaxID=30227;
                                                                                                                                                                                                                                                                                                                                                            "Repid purification and N-terminal amino acid sequence of photoaffinity-labeled juvenile hormone binding protein moth larva, Platyprepla virginalis.";
Insect Biochem. 20:801-807(1990).
-!- FUNCTION: PREVENTS JUVENILE HORMONE FROM BEING HYDROGENERAL ESTERASES BY COMBINING WITH IT SPECIFICALLY, NON. TER.
-1. SUBCELLULAR LOCATION: SECRETED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tsolas O., Sun S.C.;

Tsolas O., Sun S.C.;

Tsolation of a peptide containing a histidinyl-cysteinyl sequence from the active center of transaldolase.";

Arch. Biochem. Biophys. 167:525-533 (1975).

-i. FUNCTION: TRANSALDOLASE IS IMPORTANT FOR THE BALANCE OF METABOLITES IN THE PENTOSE-PHOSPHATE PATHWAY.

-i. CATALYTIC ACTIVITY: SEDOHEPPULOSE 7-PHOSPHATE + D-GLYCERALDEHYDE 3-PHOSPHATE = D-ERYTHROSE 4-PHOSPHATE + D-FRUCTOSE 6-PHOSPHATE.

-i. PATHWAY: NONOXYDATIVE PART OF THE PENTOSE-PHOSPHATE PATHWAY.

-i. SIMILARITY: BELONGS TO THE TRANSALDOLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
JUVENILE HORMONE-BINDING PROTEIN (FRAGMENT).
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PIR; A11497; A11497
InterPro; IPR001588; Transaldolase.
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RESULT 5
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X-RAY CRYSTALLOGRAPHY (1.1 ANGSTROMS).

MEDLINE=98376423; PubMed=9708977;

Hu S. H., Loughnan M., Miller R., Weeks C.M., Blessing R.H.,

Alewood P.F., Lewis R.J., Martin J.L.;

"The 1.1-A resolution crystal structure of [Tyr15]EpI, a novel alpha-conotoxin from Conus episcopatus, solved by direct methods.",

alpha-conotoxin from Conus episcopatus, solved by direct methods.",

-i- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY INHIBIT THEM. THIS PEPTIDE BLOCKS MAMMALIAN NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS ACETYLCHOLINE RECEPTORS (NACHR) AND THUS ACETYLCHOLINE RECEPTORS ON POSED OF ALPHA-3/BETA-2 AND ALPHA-
                                                                                                                               Postsynaptic neurotoxin;
Venom; Sulfation; 3D-str
                                                                                                                                                        PDB;
                                                                                                                                                                                                                                                                                                                                                          P56638;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
ALPHA-CONTOXIN EPI.
                                                                                                                                                                                                                                                                                                                                        Conus episcopatus (Bishop's cone)
Eukaryota; Metazoa; Mollusca; Gas
                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=88764;
                                                                                                                                                                                                                                                                                                                                  Neogastropoda;
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PROTEIN IS: 7.2, ITS MW IS:
SWISS-2DPAGE; P30095; HUMAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-93092937; PubMed-1459097; Hughes G.J., Frutiger S., Paquet N., Resanchez J.-C., James R., Tissot J.-D., Hochstrasser D.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Plasma protein map: an update by microsequencing."; Electrophoresis 13:707-714(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
UNKNOWN PROTEIN FROM 2D-PAGE OF PLASMA (SPOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Plasma
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Conoidea; Conidae; Conus
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16
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60.0%;
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57
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2D-GEL Tal
               Score 22; D
Pred. No. 8.
                                                          SULFATION.
AMIDATION.
C63385F376C99B4C CRC64;
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Pred. No. 4.9e
1; Mismatches
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01-OCT-1996 (Rel. 34, I
15-JUL-1999 (Rel. 38, I
UNKNOWN PROTEIN FROM 2D
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MCA2_RHOOP
P56870;
30-MAY-2000
                 Touzet P., Riccardi F., Morin C., De Pernollet J.-C., Zivy M., de Vienne "The maize two dimensional gel prote genome analysis program.";
Theor. Appl. Genet. 93:997-1005(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aromatic
NON_TER
SEQUENCE
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"Characterization of a maleylacetate reductase encoding region

"Rhodococcus opacus ICP.";
J. Bacteriol. 180:3503-3508(1998).

-I- CATALYTIC ACTIVITY: 3-OXOADIPATE + NAD(P)(+) = 2-MALEYLACET
                                                                                                                                                                                                                         Zea mays (Maize).
Eukaryota; Viridiplantae; Streptophyta; Embryophyt
Spermatophyta; Magnoliophyta; Liliopsida; Poales;
                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1996
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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Rhodococcus composit (Noncomparis)
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20-AUG-2001
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                                                                                                                         TISSUE=Coleoptile;
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SIMILARITY: BELONGS TO THE IRON-CONTAINING ALCOHO
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PATHWAY: 3-CHLOROCATECHOL DEGRADATION (BETA-KETOADIPATE PATHWAY)
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PS00060;
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ADH_IRON_2;
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, Last annotation update)
2D-PAGE OF ETICLATED COLEOPTILE
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2D-GEL
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Pred. No. 1.1e+03
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UC13_MAIZE
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P42997;
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Theor. Appl. Genet. 93:99/-1003(+220).
Theor. Appl. Genet. 93:99/-1003(+220).
Theor. Appl. Genet. 93:99/-1003(+220).
The MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THE PROTEIN IS: 6.8, ITS MM IS: 56.9 KDA.
THE MAISTER TO GLICOSE-6-PHOSPHATE 1-DEHYDROGENASES Maize-2DPAGE; P80619; COLEOPTILE.
                                                                                                                                                                                                                                                                                                                                                                                          Touzet P., Riccardi F., Morin C., Damerval C., Hu
pernollet J.-C., Zivy M., de Vienne D.;
"The maize two dimensional gel protein database:
genome analysis program.";
Theor. Appl. Genet. 93:997-1005(1996).
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Scyliorhinidae; Scyliorhinus.
NCBI_TaxID=7830;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
UNKNOWN PROTEIN FROM 2D-PAGE OF ETIOLATED COLEOPTILE
                                                        PHASVATOCIN.
Scyliorhinus canicula (Spotted dogfish)
Eukaryota; Metazoa; Chordata; Craniata;
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Panicoideae; Andropogoneae; Zea.
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Touzet P., Riccard
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3; Mismatches
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                                              Galeoidea;
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Liliopsida; Poales; Poaceae; PACC cl
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1.1e+03;
                                                         (Spotted catshark).
Vertebrata; Chondrichthyes;
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                                              Carcharhiniformes;
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Best Local s
Matches 3
                                                                                                                                                                                                                                                                                                                                                                                      evidence condida utilis.";
Candida utilis.";
Arch. Biochem. Biophys. 178:69-78(1977).
-!- FUNCTION: TRANSALDOLASE IS IMPORTANT FOR THE BALANCE OF
METABOLITES IN THE PENTOSE-PHOSPHATE PATHWAY.
-!- CATALYTIC ACTIVITY: SEDOHEPTULOSE 7-PHOSPHATE + D-GLYCERALDEHYDE
-!- CATALYTIC B- D-ERYTHROSE 4-PHOSPHATE + D-FRUCTOSE 6-PHOSPHATE.
-!- PATHWAY: NONOXYDATIVE PART OF THE PENTOSE-PHOSPHATE PATHWAY.
-!- STMILARITY: BELONGS TO THE TRANSALDOLASE FAMILY.
                                                                                                                                                                                                                                                                   Transferase;
NON_TER
NON_TER
SEQUENCE 9
                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00958; TRANSALDOLASE_2; PROSITE; PS01054; TRANSALDOLASE_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sun S.C., Joris L., Tsolas O.;
"Purification of crystallization of transaldolase isozyme I
evidence for different genetic origin of isozymes I and III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pichia jadinii (Yeast) (Candida utilis).
Bukaryota; Fungi; Ascomycota; Saccharomycotina;
Saccharomycetales; Saccharomycetaceae; Pichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TALI_PICJA STANDARD; PRT; 9 AA. P17440; P17440; O1-AUG-1990 (Rel. 15, Created) O1-AUG-1990 (Rel. 15, Last sequence update) O1-FEB-1994 (Rel. 28, Last annotation update) TRANSALDOLASE I (EC 2.2.1.2) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=77110646;
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11
                                                                                                                                                                            Local
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hormone;
DISULFID
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MEDLINE=95062247;
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2; Conserv
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FE; PS00264; NEUROHYPOPHYS_HORM; 1.
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3; Conserv
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17EDD76EB44449DB CRC64;
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Pred. No. 1e+05;
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Best Local S
Matches 3
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Proc. Natl. Acad. Sci. U.S.A. 92:9358-9362(1995).

-!- FUNCTION: CATALYZES THE REMOVAL OF ELEMENTAL SULFUR ATOMS FROM CYSTEINE TO PRODUCE ALANINE. SEEMS TO PARTICIPATE IN THE BIOSYNTHESIS OF THE NITROGENASE METALLOCLUSTERS BY PROVIDING THE BIOSYNTHER REQUIRED FOR THE FE-S CORE FORMATION (BY
                                                                                  This
                                           between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=96016168; PubMed=7568132;
Thiel T., Lyons E.M., Erker J.C., Er
"A second nitrogenase in vegetative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NISI_ANASQ STANDARD; PRT; 15(244507; Q44507; 20-AUG-2001 (Rel. 40, Created) 20-AUG-2001 (Rel. 40, Last sequence upda 20-AUG-2001 (Rel. 40, Last annotation                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. Monnerjahn U., Boe
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PROTEIN IS: 4.77, ITS MW IS:
SWISS-2DPAGE; P34990; HUMAN.
NON_TER 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUB-Erythrocyte;
Golaz O., Hughes G.J., Frutiger S., Paquet N.,
Pasquali C., Sanchez J.-C., Tissot J.-D., Apperature of the Control of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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Ol-FEB-1994 (Rel. 28, Created)
Ol-FEB-1994 (Rel. 28, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
UNKNOWN PROTEIN FROM 2D-PAGE OF RED BLOOD CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     _HUMAN
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Submitted (FEB-1994) to the SWISS-PROT data
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Mammalia; Eutheria;
                                                                                                    COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).

SUBUNIT: HOMODIMER (BY SIMILARITY).

MISCELLANBOUS: BELONGS TO THE NIF1 GENE CLUSTER WHICH IS EXPRESS IN HETEROCYSTS UNDER ANABROBIC AND AEROBIC CONDITIONS.

SIMILARITY: BELONGS TO CLASS-V OF PYRIDOXAL-PHOSPHATE-DEPENDENT AMINOTRANSFERASES. NIFS/ISCS SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                 SWISS-PROT entry is copyright.
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etazoa; Chordata; Craniata; Vertebrata; F
theria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Boehme H. -1992) to
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jht. It is produced through a collaboration
Bloinformatics and the EMBL outstation -
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ve cells of
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(NITROGENASE METALLOCLUSTERS
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Homo.
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RESULT 14
UR2_SCYCA
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                                P35490;
P35490;
P35490;
P35490;
O1-JUN-1994 (Rel. 29, Careated)
O1-JUN-1994 (Rel. 29, Last sequence update)
O1-JUN-1994 (Rel. 40, Last annotation update)
UROTENSIN II (U-II) (UII).
Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
Scyliorhinus canicula (Spotted dogfish) (Partebrata; Chondrichthyes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P07495;
01-APR-1988 (Rel. 07, Created)
01-APR-1988 (Rel. 07, Last sequence update)
01-APR-1990 (Rel. 14, Last annotation update)
BOMBOLITIN IV.
Pennsvlvanicus (American common
Elasmobranchii; (
Scyliorhinidae; S
NCBI_TaxID=7830;
[1]
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**Bombolitins, a new class of mast cell degranulating the venom of the bumblebee Megabombus pennsylvanicus.

J. Biol. Chem. 260:1437-1444(1985).

-i. FUNCTION: MAST CELL DEGRANULATING PEPTIDE.

PIR; D22595; D22595.

Mast cell degranulation; Venom.

**SEQUENCE 17 AA; 1873 MW; A34A43514BCFDFB6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000192; Aminotransf_class_V.
PROSITE: PS00595; AA_TRANSFER_CLASS_5; PARTIAL.
Nitrogen fixation; Lyase; Pyridoxal phosphate.
NON_TER 15 15
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use by non-profit institutions as 1 modified and this statement is not rem
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoldea; Apidae; Bombus.
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                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE.
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3; Conserv
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                         Scyliorhinus
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33.3%;
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P81362;
15-JUL-1998
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                                  1TRB_ALBJU
P24927;
01-MAR-1992
01-MAR-1992
01-JUN-1994
01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
01-JUN-1994 (Rel. 29, Last sanctation update)
01-JUN-1994 (Rel. 29, Last sanctation update)
TRYPSIN INHIBITOR B CHAIN (FRACMENT).
Albizzia julibrissin (Silk tree).
Eukaryota; Viridiplantae; Streptophyta; Embry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                  Flengsrud R., Skjeldal L.;
"Two-dimensional gel electrophoresis separation and sequence analysis of proteins from Clostridium paste Electrophoresis 19:802-806(1998).
-i- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OPROTEIN IS: 5.4, ITS MW IS: 38.2 KDA.
                                                                                                                                                                                                                                                                                                                                                                                               Clostridium pasteurianum. Bacteria; Firmicutes; Bac Clostridium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conlon J.M., O'Harte F., Smith D.D., Balment R.J., Hazon "purification and characterization of urotensin II and pa from an elasmobranch fish, Scyliorhinus canicula (common Neuroendocrinology 55:230-235(1992).

-i- FUNCTION: HAS A SUGGESTED ROLE IN OSMOREGULATION AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE.
TISSUE-Spinal cord;
MEDLINE-92319231; PubMed=1620290;
Conlon J.M., O'Harte F., Smith D.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-1998 (Rel. 36, Creat
15-JUL-1998 (Rel. 36, Last
15-JUL-1998 (Rel. 36, Last
UNKNOWN PROTEIN CP 46 FROM
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MUSCLE STIMULATION.
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PE; PS00984; UROTENSIN_II; 1.
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 Streptophyta; Embryophyta; Tracheophyta;
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annotation updat
2D-PAGE (FRAGMEN
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Pred. No. 1.9e
1; Mismatches
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RESULT 18
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DE FIBRIN
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SEQUENCE
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01-JAN-1990 (Rel. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Blomback B., Blomback M., Grondahl N.J.;
"Studies on fibrinopeptides from mammals.",
Acta Chem. Scand. 19:1789-1791(1965).
-i-FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIEL
POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euf
Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae;
NCBI_TaxID-9667;
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"Proteinase inhibitors from a mimosoideae legume, Albizzia
julibrissin. Homologues of soybean trypsin inhibitor (Kunitz)
J. Biochem. 86:1795-1805(1979)
-!- FUNCTION: INHIBITS TRYPSIN AND ALPHA-CHYMOTRYPSIN.
-!- SUBUNIT: HETERODIMER OF AN "A" AND A "B" CHAIN LINKED BY
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NCBI_TaxID=3813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGGREGATION.

SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS (ALPHA, BETA, & GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B TROM ALPHA & BE CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
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SIMILARITY: TO BETA CHAINS
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Ikenaka T.;
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"Isolation, identification and synthesis of locuste
additional neuropeptide of Locusta migratoria. Memb
cephalomyotropic peptide family.";
Insect Biochem. 20:479-884(1990).
-I- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE
(MYOTROPIC ACTIVITY).
-I- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local (
Matches
                                                                                                                                                                                                                                                                                      - v1-Aug-1991 (Rel. 19, Created)
T 01-AUG-1991 (Rel. 19, Last sequence update)
T 01-AUG-1991 (Rel. 19, Last annotation update)
LOCUSTAMYOTROPIN 2 (LOW-NHT-2),
LOCUSTAMYOTROPIN 2 (LOW-NHT-2),
LOCUSTAMYOTA; Metazoa; Arthropoda; Tracheata; Hexa
Pterygota; Neoptera; Orthopteroidea; Orthoptera
Acridomorpha; Acridoidea; Acrididae; Locusta.
NCBI_TaxID=/004;
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TISSUE-Lary;
TISSUE-Lary;
X MEDLINE-98054539; PubMed=9392829;
A Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley
Davey M., East P.D., Thorpe A.;
T "Lepidopteran peptides of the allatostatin superfamily.";
L Peptides 18:1301-1309(1997).
- 1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
W Neuropeptide; Amidation.
T MOD_RES
B AMIDATION.
SEQUENCE 8 AA; 934 MW; C82879C45B51F775 CRC64;
                                                                                                    Neuropeptide;
MOD_RES
SEQUENCE 8 A
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PROSITE; PS00539; PYROKININ; 1
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30-MAY-2000 (Rel. 3
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CYDIASTATIN 1.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Tortricoidea; Tortricidae; Olethreutinae; Cydia.
3 DFTPRL
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NCBI_TaxID=82600;
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26341771A9CAA87B CRC64;
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Pred. No. 1e+0
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idea; Orthoptera; Cael
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AC Q10584;

AC Q10584;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE HEMOCYANIN B CHAIN (KLH-B) (FRACMENT).

OS Megathura crenulata (Giant keyhole limpet).

OC Eukaryota; Metazoa; Mollusca; Gastropoda; Archaeogastropoda;

Dartellacea; Patellidae; Megathura.
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HCYB_MEGCR
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Matches 4
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01-OCT-1994
15-JUL-1998
                   Swerdlow R.D., Ebert R.F., Lee P., Bonaventura C., Miller K.I.; "Reyhole limpet hemocyanin: structural and functional characterization of two different subunits and multimers."; Comp. Biochem. Physiol. 113B:537-548(1996).

-i- FUNCTION: HEMOCYANINS ARE COPPER-CONTAINING OXYGEN CARRIERS OCCURRING FREELY DISSOLVED IN THE HEMOLYMPH OF MANY MOLLUSK:
                                                                                                                                                        Orconectes limosus (Spinycheek crayfish).
Eukaryota; Metazoa; Arthropoda; Crustacea
Eumalacostraca; Eucarida; Decapoda; Pleoc
Restacostraca; Cambaridae; Orconectes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000896; Hemocyanin.
PROSITE; PS00209; HEMOCYANIN_1; PARTIAL.
PROSITE; PS00210; HEMOCYANIN_2; PARTIAL.
                                                                                                                                                                                                           ORCOKININ
                                                                                                                                                                                                                                                                         ORCK_ORCLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                      SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Respiratory protein; Oxygen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          demolymph.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BIOTECHNOLOGY: POTENT IMMUNOGEN USED CLASSICALLY AS A CARRIER PROTEIN FOR HAPTENS AND MORE RECENTLY IN HUMAN VACCINES AND FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROTEIN FOR HAPTENS AND MORE RECENTLY IMMUNOTHERAPY OF BLADDER CANCER. SIMILARITY: BELONGS TO THE TYROSINASE
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SUBUNIT: DIDECAMERS AND EXTENDED MULTIMERS
          TISSUE
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4; Conserv
          SPECIFICITY: ABDOMINAL NERVE CORD AND HINDGUT
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Pred. No.
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                                                                                                                                                                      Pleocyemata;
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UP51_UPEIN
P82036;
30-MAY-2000
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01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bradford A.M., Raftery M.J., Bowie J.H., Adams G.W., Severini C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachi
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                                                                                                                                                                                                                                        Psophocarpus scandens.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid Spermatophyta; Magnoliophyta; Paracoliophyta; Magnoliophyta; Magnoliophyt
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SEQUENCE 13 1
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                                  Psophocarpus scandens.";
Phytochemistry 27:2847-2855(1988).
-!- SUBUNIT: DIMER OF TWO IDENTICAL OR NEARLY
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                                                                                                             Kortt A.A.;
                                                                                                                                 TISSUE-Seed;
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                                                                                                                                                                                        Psophocarpus.
NCBI_TaxID=3890;
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                                                                                                                                                                                                                                                                                                           BASIC LECTIN B1 (FRAGMENT).
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                                                                                         "Isolation and characterization of
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P2285;

01-AUG-1991 (Rel. 19, Created)
01-AUG-1994 (Rel. 19, Last sequence update)
01-CCT-1994 (Rel. 30, Last annotation update)
BASIC LECTIN B2 (FRAGMENT).
Psophocarpus scandens.
*Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosid
eurosids I; Fabales; Fabaceae; Papillonoideae; Phaseoleae;
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P22582;
01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last seq
01-AUG-1998 (Rel. 36, Last ann
ACIDIC LECTIN A1 (FRAGMENT).
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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SIMILARITY: WITH P.TETRAGONOLOBUS BASIC LECTINS IN N-TERMINAL SEQUENCE, AA COMPOSITION, ERYTHROCYTE AND SUGAR SPECIFICITIES, PA0007.
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Search completed: Job time: 183 sec

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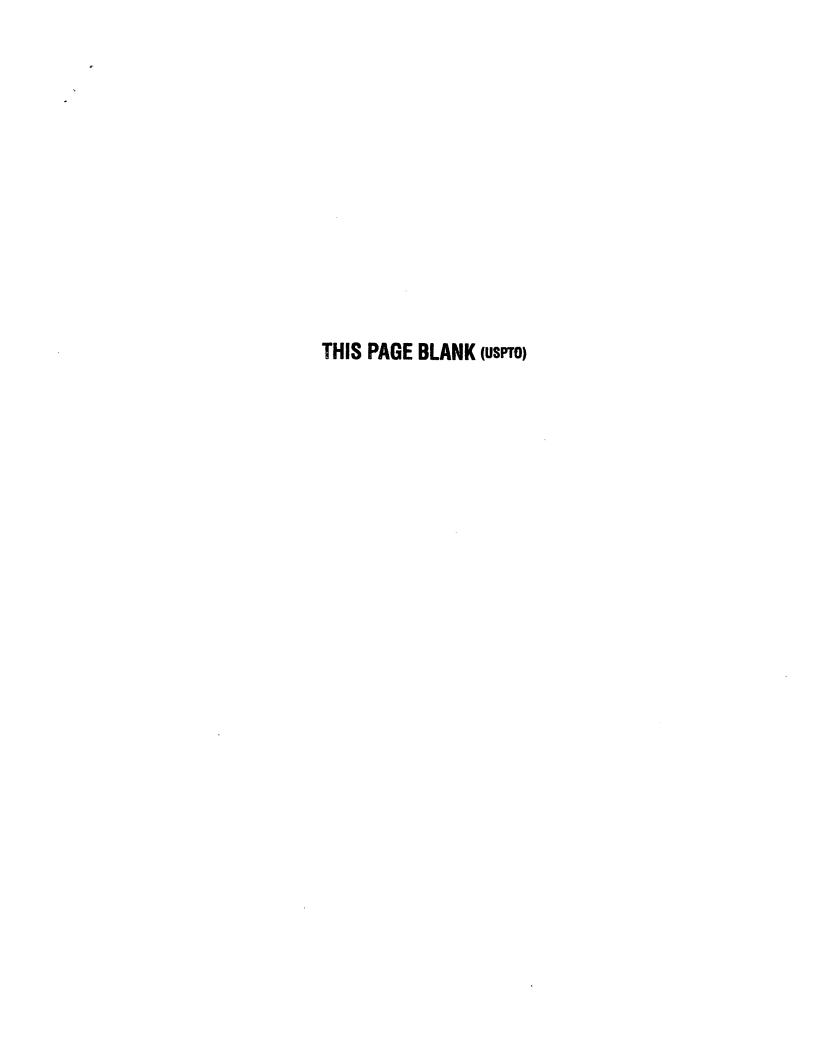
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-!- PTM: CONTAINS ABOUT 9% CARBOHYDRATE. HETEROGENEITY IN CARBOHYDRATE COMPOSITION MAY RESULT IN DIFFERENT ISOLECTIN FORMS.
-!- SIMILARITY: WITH P.TETRAGONOLOBUS BASIC LECTINS IN N-TERMINAL SEQUENCE, AA COMPOSITION, ERYTHROCYTE AND SUGAR SPECIFICITIES.
-PIR: PA00008; PA00008.
                                                                                                                                              SEQUENCE 15
                                                                                                                                                                                         Kortt A.A.;
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NCBI_TaxID=3890;
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(c) 1993 - 2000 Compugen Ltd
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Q5574 homo sapien
Q77922 oreochromis
Q99qex2 human immun
Q96417 drosophila
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P97622 rattus norv
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ALIGNMENTS

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RESULT
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Best Local Similarity
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 Q9PRW2;
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"Isolation of multiple isoforms of alpha-fibrinogenase from the Western diamondback rattlesnake, Crotalus atrox: N-terminal sequence homology with ancrod, an antithrombotic agent from Malayan viper."; Biochem. Biophys. Res. Commun. 201:1414-1423(1994).

SEQUENCE 15 AA; 1640 MW; 03EFE10227CA12DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9PRW3 PRELIMINARY; PRT; 15 AA.
Q9PRW3;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
ALPHA-FIBRINOGENASE ISOFORM A2 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                      Crotalus atrox (Western diamondback rattlesnake).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Pred. No. 1.3e+03;
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                                                                                                                                                                          MEDLINE=95072587; PubMed=7526926; Yamanishi K., Matsuki M., Konishi K., "A novel mutation of Leul22 to Phe at residue in the helix initiation motif
                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

MEDINE-92005680; PubMed=1717157;

COulombe P., Hutton M., Letai A., Hebert A., Paller A., Fuch
"Point mutations in human keratin 14 genes of epidermolysis
simplex patients: genetic and functional analyses.";

[2]
                                                                                                                                                   bullosa simplex.";
Hum. Mol. Genet. 3:1171-1172(1994).
                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
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Homo sapiens (Human).
Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606
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MEDLINE=94296418; PubMed=8024586;

Hung C.C., Chiou S.H.;

"Isolation of multiple isoforms of alpha-fibrinogenase from the Mestern diamondback rattlesnake, Crotalus atrox: N-terminal sequence homology with ancrod, an antithrombotic agent from Malayan viper.";

Biochem. Biophys. Res. Commun. 201:1414-1423(1994).

SEQUENCE 15 AA; 1656 MW; 03EFE10227D52FDA CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
Crotalus atrox (Western diamondback rattlesnake).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Crotalus.
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a highly conserved hydrophobic
of keratin 14 in epidermolysis
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SEQUENCE
                                                                                                                      Pourmann M., Froger N., Brunel D.;

"Amplified consensus gene markers: Tools designing for a of Arabidopsis known function genes in Brassica.";

Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AF229413; AAK00685.1;
                                                                                                                                                                                                               Brassica napus (Rape).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; eurosids II; Brassicales; Brassicaceae; Brassica.
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01-JUN-2001 (Tremblrel. 17
01-JUN-2001 (Tremblrel. 17
PHYTOCHROME A (FRAGMENT).
                                                                                                                                                                                  STRAIN=CV.
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                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                   Local
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MEDILUS-88018019; PubMed-3659919;
Chen S.H., Habib G., Yang C.Y., Gu z
Silberman S.R., Cai S.J., Deslypere
Li W.H., Chan L.;
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         8 DVTTRLREN
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01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
APOLIPOPROTEIN B48 (FRAGMENT).
APOB.
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Q9AXV9;
01-JUN-2001
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Q9FSA9;
01-MAR-2001
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"Amplified consensus gene markers: Tools designing for a of Arabidogsis-known-function genes in Brassica.";

Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AF229417; AAK00689.1; -...

NON_TER 16 16
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NCBI_TaxID-3712;
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"Inferring the history of the polyploid Silene aegaea
"Inferring the history of the polyploid Silene aegaea
(Caryophyllaceae) using nuclear and chloroplast DNA sequence
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL: AJ296130; CAC13014.1; -.
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Silene aegaea.
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P97622;
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                                                                                                                                                                                                                EMBL; MI
                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=92201692; PubMed-1551590;
Rhiel E., Stirewalt V.L., Gasparich
"The psaC genes of Synechococcus sp.
cloning and sequence analysis.";
                                                                                                                                                                                                                                                                                               PUTATIVE ORF1 (FRAGMENT)
Synechococcus sp.
Bacteria; Cyanobacteria;
NCBI_TaxID=1131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Adams L.A., Werny I., Schwar Submitted (CCT-1996) to the EMBL; U75408; AAB19110.1; -. HSSP; P02791; 1AEW. NON_TER 13 13
                                                                                                                                                                                                                       Gene 112:123-128(1992).
EMBL; M86238; AAA27351.
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01-NOV-1998
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STRAIN=WISTAR-KYOTO; TISSUE=AORTIC
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                                                                                                                                                                                                       SEQUENCE
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Homo sapiens (Human)
Eukaryota; Metazoa;
                                                                                                                     7 DVTGRLQ 13
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3; Conservative
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2.5e+03;
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 Vertebrata;
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; Murinae; Rat
  Euteleostomi;
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Mammalia;

Nucleic Acids Res. SEQUENCE FROM N.A.

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SEQUENCE FROM N.A.

MEDLINE-98315113; PubMed=9649539;

Malaga-Trillo E., McAndrew B., Vincek V., Zaleska-Rutczynska Z.,

Sueltmann H., Figueroa F., Klein J.;

"Linkage relationships and haplotype polymorphism among cichlid class II B loci.";
                                                                                                                                                                                                                                                                    Ol-NOV-1998 (TremBLrel 08, Created)
Ol-NOV-1998 (TremBLrel 08, Last sequence update)
OreoChromis niloticus (Nile tilapia) (Tilapia nilotica).
OreoChromis niloticus (Nile tilapia) (Tilapia nilotica).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Meopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;
Cichlidae; OreoChromis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-FETAL LIVER;
MEDLINE-8515492; PubMed-6085063;
Urano Y., Sakai M., Watanabe K., Tamaoki T.;
"Tandem arrangement of the albumin and alpha-fetoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-FETAL LIVER;

MEDLINE-82105994; PubMed-6275391;

Dugaiczyk A., Law S.W., Dennison

""" aride sequence and the enco
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TISSUE-FETAL LIVER;
MEDLINE-82081882; PubMed=6171778;
Lawn R.M., Adelman J., Book S.C., Franke A.E.,
Najarian R.C., Seeburg P.H., Wion K.L.;
"The sequence of human serum albumin cDNA and i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                McMBI_TaxID=9606;

MCBI_TaxID=9606;
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d the encoded amino acids
                              Score 22; DB
Pred. No. 4.2e
1; Mismatches
                                                                                            A56619E46BAB5F2D CRC64;
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Pred. No. 4.7e+05;
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Best Local
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NON_TER 9
SEQUENCE 9 AA; 1089
                                                                                                                                                               Erickson J.W., Cline T.W.;
"Key aspects of the primary sex determination across the genus Drosophila.";
Development 125:3259-3268(1998).
                                                                                                                                                                                                                                                                                                                                                       01-MAY-1999
01-MAY-1999
01-JUN-2001
                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=98337843; PubMed=9671597;
Erickson J.W., Cline T.W.;
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Q9QEX2;
PKBLILL...
Q9QEX2;
O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-MAY-2000 (TrEMBLrel. 13, Last annotation update)
ENVELOPE GLYCOPROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                      Drosophila virilis (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Trachea
Pterygota; Neoptera; Endopterygota; Dip
Ephydroidea; Drosophilidae; Drosophila.
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Lin H.J., Slawak E.B., Hollinger F.B.;
"Mutation rate of human immunodeficiency virus type 1 ger
deduced from long term culture of its biological clones.
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF178668; AAF04374.1;
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Viruses; Retroid viruses; Retrovir
NCBI_TaxID=11676;
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Score 21; DB 5; Le
Pred. No. 4.7e+05;
1; Mismatches 1;
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Pred. No. 4.5e+03;
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ota; Diptera; Brachycera; Muscomorpha;
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PRELIMINARY;

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22.9%; 50.0%;

NON_TER SEQUENCE EMBL;

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human genome. Gene 32:255-2

:255-261(1984).

L00133;

AAC95394.1;

SEQUENCE FROM N.A

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NCBI_TaxID=8128;

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Submitted (SEP-199) to the E
EMBL; AF185778; AAF05483.1;
EMBL; AF185771; AAF05484.1;
EMBL; AF185772; AAF05485.1;
EMBL; AF185773; AAF05486.1;
EMBL; AF185774; AAF05486.1;
EMBL; AF185775; AAF05488.1;
EMBL; AF185775; AAF05489.1;
EMBL; AF185776; AAF05489.1;
EMBL; AF185776; AAF05489.1;
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Q9TQV4;
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Mammalia; Eutheria; Perissodactyla; Equidae;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
POP-VARIANT * TRANSFERRIN GENE, EXON 17 AND PARTIAL
                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae; Caryophyllales; Caryophyllaceae; Silene.
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01-MAR-2001
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                                                                                                                                                   "Oppp M., Oxelman B.;
"Inferring the history of the polyploid Silene aegaca (Caryophyllaceae) using nuclear and chloroplast DNA seq. (Caryophyllaceae) using nuclear and chloroplast DNA seq. (Caryophyllaceae) using the EMBL/GenBank/DDBJ databases
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Q9TRU1;
01-MAY-2000 (
01-MAY-2000 (
01-MAY-2000 (
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P82437;
O1-JUN-2000
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                                                                                                                                   NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                  STRAIN-CV. PETIT HAVANA;
Blee K.A., Bonham V.A., Mitche
Blee K.A., Bonham V.A.,
Wojtaszek P., Bolwell G.P.;
"Proteomic study of secondary
                                                                                                                                                                                                                                                                                                                                                                                  Nicotiana tabacum (Common tobacco):
Eukaryota; Viridiplantae; Streptophyta; Embryophyta
Spermatophyta; Magnoliophyta; eudicotyledons; core
Asteridae; euasterids I; Solanales; Solanaceae; Nic
NCBI_TaxID=4097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               veiby O.P., Sletten K., Husby G.,
"Amino acid sequence analyses of of bovine kidney.";
scand. J. Immunol. 35:63-69(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Ch
Mammalia; Eutheria; Ce
Bovidae; Bovinae; Bos.
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01-MAY-2000 (TrembLrel.
01-MAY-2000 (TrembLrel.
43 KDA CYANOGEN BROMIDE
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01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
26 KDA CELL WALL PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                tobacco culture.";
Planta 0:0-0(2000)
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                                                                                                                                                                         Cell wall.
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4; Conservative
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1257 MW; 0D5C94FDE9B76AA4 CRC64;
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Q9FSA8;
01-MAR-2001 (TrEMBLrel. 16, C;
01-MAR-2001 (TrEMBLrel. 16, L;
01-MAR-2001 (TrEMBLrel. 16, L;
RNA POLYMERASE II (FRAGMENT).
                                                                                                                                               Popp M., Oxelman B.;
"Inferring the history of the polyploid Silene aegaea (Caryophyllaceae) using nuclear and chloroplast DNA sequence data. Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ296139; CAC13015.1; -
                                                                                                                                      NON_TER
                                                                                                                                                                                                                                                                               Silene baccifera (Berry catchfly) (Cucubalus baccifer). Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae; Caryophyllales; Caryophyllaceae; Silene.
                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                            NCBI_TaxID=54818;
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Q9UNV6;
Q1-MAY-2000
Q1-MAY-2000
Q1-OCT-2000
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EMBL; AF085628; AAD22141.1; -.
EMBL; AF085627; AAD22141.1; JOINED.
HSSP; P29218; 11MB.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yoshikawa T., Turner G.,
Detera-Wadleigh S.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE=97463449; PubMed=9322233;
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01-MAX-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
INOSINE MONOPHOSPHATASE 2 (FRAGMENT).
     6 FNDVT 10
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les 3; Conserv
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80.0%;
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                                            Score 21;
Pred. No.
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Last annotation update)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae; Caryophyllales; Caryophyllaceae; Silene.

NCBI_TaxID=49735;
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SEQUENCE FROM N.A.
Oxelman B.;
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EMBL; AJ296131; CAC13023.1; -.
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EMBL; AJ296105; CAC13028.1; -.
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Eukaryota; Viridiplantae;
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Search completed: Job time: 197 sec

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14: /SIDSB/gcgdata/geneseq/geneseqp/AA1993.DAT:*
15: /SIDSB/gcgdata/geneseq/geneseqp/AA1995.DAT:*
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Copyright (c) 1993 - 2000 Compugen
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Cadherin-8 cell ad
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Virus infection fa
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Viral integrase in Cadherin-8 cell ad Thrombopoietin rec	nomadura sp. nomadura fle	Human CXCR3 immuno Mucor hiemalis end	20 pr	Stearoy1~VIP(1-14) Vasoactive Intesti	ω	gp120 protein	ntibod	Random peptide #/	antibody	Ε	facto	рe	D peptide	Ū	in-assoc	gene	d AU	of.	of	ronic ac		Human platelet gly .	Lepidoptera allost	intera	Mycoplasma genital	micro	Hexapeptide #5 wit	Human serum albumi	Human serum albumi	۳.	Human leucocyte an	Metal-regulated tr

ALIGNMENTS

RESULT AAB67300

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20-APR-2001 (first entry)

AAB67300;

AAB67300 standard; Peptide; 16

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Sakanaka M, Tanaka
                                                                                                                           Cytokine peptide #6
WPI; 2001-204263/21
                       (SAKA/) SAKANAKA M.
(TANA/) TANAKA J.
(SATO/) SATO K.
                                                 30-JUN-1999;
                                                            30-JUN-2000; 2000EP-0305504.
                                                                          31-JAN-2001.
                                                                                      EP1072609-A2.
                                                                                                  Homo sapiens
                                                                                                               Prosaposin; cell death; Bcl-XL; brain; cardiac muscle
                                                 99JP-0185155
            ŗ
            Sato
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            Morita F,
            Sadamoto Y;
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RESULT
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JD ANY 58596
AC ANY 58596
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mammals, including humans. SAG1 is anchored to the plasma membrane of T. gondii via a GPI (glycosylphosphatidylinositol) anchor, which is attached to the C-terminal anchor region (residues 308-336). The invention provides a truncated SAG1 protein, which lacks the anchor region and comprises amino acids 48-307, and a SAG protein N-terminally fragments can be used in the manufacture of a subunit vaccine for the Toxoplasma vaccine is available, but cannot be administered to humans due to, the risk of reversion of the attenuated strain to a virulent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                 The invention relates to the recombinant production of the toxoplasma antigen SAG1 or a fragment thereof in the yeast Pichia pastoris. SAG1 is the major surface antigen of Toxoplasma gondii, an obligate intracellular protozoan parasite responsible for toxoplasmosis in
                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Page 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biemans R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SMIK)
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15-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               epitope; antibody
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY58596 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to use of a prosaposin-related peptide or derivative, in the production of a medicament for use in preventing or delaying cell death, or in promoting the expression of cell death supporting gene product Bcl-XL. The invention is useful for preventing the death of cells e.g. brain cells, neurons and cardiac muscle cells, in vitro or ex vivo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 production of toxoplasma antigen SAG1 for use in vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bollen A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16
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99GB-0008564.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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QУ

6 FNDVTTRL 13

Query Match Best Local S Matches 7

Similarity 7; Conserv

33.3%;

Score 32; Pred. No.

Conservative

0;

Mismatches

1.1e+02; 1;

Length 15;

Indels

0;

Gaps

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AAR83971
IID AARR
XX
AC AARE
XX
AC AARE
XX
AC AARE
XX
Viri
KW AMir
KW PHO;
XX
PHO;
YA
PA (KA:
YX
PR (Z-1
XX
PT Inf(
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CC AAR)
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CC C CL
CC C CCL
CC C Vie
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
Sequence
                                                         AAR83791 is an amino-terminal peptide of a virus infection factor derived from heat-treated silkworm body fluid. The new virus infection factor (VIF) is useful for promoting the infection of insect cells with recombinant nuclear polyhedrosis virus. The virus having been recombined with a useful protein-expressing gene. The insect been recombined with a useful protein-expressing the insect that it is the combined with a useful protein-expressing gene. The insect been recombined with a useful protein-expressing the insect that it is the combined with a useful protein-expressing gene. The insect that it is the combined with a useful protein-expressing gene.
                                              yields.
                                                                                                                                                                                                    Virus infection factor from silkworm body fluid infection of insect cells with protein-expressing
                                                                                                                                                                    Claim 6;
                           isoelectric point
                                                                                                                                                                                                                                                         WPI; 1995-371176/48
                                                                                                                                                                                                                                                                                       (KATA )
                                                                                                                                                                                                                                                                                                                    22-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Virus
                                                                                                                                                                                                                                                                                                                                                                               03-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                            JP07252298-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Amino
                                                                                                                                                                                                                                                                                                                                                 18-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Philosamia cynthia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          form. Prior art recombinant expression of SAG1 has been attempted in Escherichia coli, mammalian cells or S. cerevisiae, but has been associated with problems such as misfolding and insolubility, low yields of correctly folded SAG1, or heterogeneous protein production. In difficult and time-consuming, due to the GPI anchor. Sequences AAY58595-Y58596 represent peptide epitopes of T. gondii SAG1, which were used to raise polyclonal antibodies in an exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    recombinant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR83971;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR83971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                               culture medium
               The new VIF has a mol. wt. of approx. 15.2 kDa and ectric point of 9 or higher.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 CN---FNDVTTRLREN 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cneksfkdilpklten
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            terminal; silkworm; virus infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               infection
                                                                                                                                                                                                                                                                                  KATAKURA IND CO LTD
                                                                                                                                                               Page 2; 11pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard; peptide;
 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16
AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 high yield; body fluid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first
                                                                                                                                                                                                                                                                                                                 93JP-0314038
                                                                                                                                                                                                                                                                                                                                             94JP-0308468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        factor N-terminal peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                     ricini
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33.9%;
                                                                                                                                                            Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 32.5; DB
Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          factor; promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from silkworm body fluid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4;
                                                                                                                                                                                                    recombinant viru
                                                                                                                                                                                                                    used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ω
••
                                                                                                                                                                                                 virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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RESULT
AAW30024
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ID AAR7
                                                                                                                                       Query Match
Best Local Similarity
"hes 5; Conserv
  DЬ
                                                                                                                              Ş
                                                                                                                                                                                            RESULT
                                                                                                                                                                                                        The peptide given in AAR70773, corresponding to amino acids 8-29 o human saposin-C (AAR70784), promotes neurite outgrowth in vitro. A consensus sequence was determined by comparing the peptide with hematopoietic and neuropoietic cytokines, and neurotrophic peptide (AAR70774-82) were identified in the AB loop of human ciliary neurotrophic factor, interleukins-6, -2, -3 and -gamma, erythropoietin and leukocyte inhibitory factor, and in helix C of interleukin-1-beta and oncostatin-M. Prosaponin (AAR70783) and saposin-C also promoted nerve cell myelination ex vivo.
                                                                                                                                                                                                                                                                                                             Stimulating neural cell out-growth and myelination - with pro:saposin, saposin C or new neurotrophic peptide(s) from cytokine(s), for treating nervous system diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Erythropoietin; EPO; cytokine; myelination; nervous system; neurotrophic peptide; multiple sclerosis; leukoencephalitis; adrenal leukodystrophy; neuroblastoma.
                 Cytokine hEPO AB loop derived peptide.
                                   14-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR70779;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR70779 standard; Peptide; 16
                                                                    AAW30024 standard; peptide; 17
                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                 WPI; 1995-082029/11.
                                                                                                                                                                                                                                                                                                                                                                                  (OBRI/) OBRIEN J S.
                                                                                                                                                                                                                                                                                                                                                                                                   30-JUL-1993;
21-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                            28-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                              09-FEB-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9503821-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EPO neurotrophic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-AUG-1995
                                                                                                               |||: |: |
2 ehcslnenit 11
                                                                                                                              2 EHCNFNDVTT 11
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                                                                                                                                                                                           16
                                                                                                                                                                                                                                                                                             Page 36; 50pp; English.
                                                                                                                                                Conservative
                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                           AA;
                                                                                                                                                                                                                                                                                                                                                                  Obrien
                                                                                                                                                                                                                                                                                                                                                                                                   93US-0100247.
94US-0232513.
                                                                                                                                                                                                                                                                                                                                                                                                                            94WO-US08453
neural disorder; demyelination
                                                                                                                                                        33.3%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                  JS;
                                                                                                                                               ?
                                                                                                                                               Score 32; DB 16;
Pred. No. 1.2e+02;
2; Mismatches
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                                                                                                                                                               Length 16
                                                                                                                                               Indels
                                                                                                                                                                                                                                                    peptides
                                                                                                                                               0,
                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                             0f
                                                                                                                                                                                                                            human
                                                                                                                                               0;
                                                                                                                                                                RESULT
AAW66142
 밁
                                                                                                                                                                                                                 δÃ
                                                            Synthetic
11-SEP-1997;
                 11-SEP-1998
                                   WO9839357-A1
                                                                            neural cell
                                                                                    prosaposin;
                                                                                                    Prosaposin receptor agonist #16.
                                                                                                                      17-NOV-1998
                                                  Homo sapiens
                                                                                                                                                                        6
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Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tissue. It can be used to stimulate neurite outgrowth, inhibit neural cell death, promote myelination or inhibit demyelination. The method is used to alleviate neuropathic pain resulting from a peripheral nerv disorder, such as neuroma, nerve compression, crush or stretch and incomplete nerve transsection, mononeuropathy or polyneuropathy. Alternatively the neuropathic pain results from a disorder of the dorsal root ganglia, spinal cord, brainstem, thalamus or cortex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      has been developed of alleviating or preventing neuropathic pain in a subject, comprising administering an effective amount of an active fragment of prosaposin to the subject. The prosaposin derived peptide is useful for therapy of neural or demyelination disorders in neural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neural cell death; inhibition; myelination; neurite outgrowth; neuropathic pain; peripheral nerve disorder; neuroma; mononeuropathy; polyneuropathy; dorsal root ganglia; spinal cord; brainstem; thalamus; cytokine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Prosaposin-derived peptide - useful for therapy of neural demyelination disorders in neural tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      O'Brien JS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9732895-A1
AAW66142;
                                                   AAW66142 standard; peptide; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents a specifically claimed cytokine derived peptide for use in the following method of the invention. A method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 16; Page 56; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-SEP-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1997-470538/43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                      2 ehcslnenit 11
                                                                                                                                                                                                                                                         2 EHCNFNDVTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 AA;
                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96US-0611307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97WO-US04143
                                                                                                                                                                                                                                                                                                                                             33.3%;
                                                                                                                                                                                                                                                                                                                        2;
                                                                                                                                                                                                                                                                                                                                                Score 32;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                             DB 18;
1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                     Length 17,
                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S,
                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nerve
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receptor agonist; neuropathic pain; neurite death; nerve disorder; side effect.

outgrowth;

0

97WO-US16062

(first entry)

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RESULT
AAX761736
ID AAX76
XX AAX76
XX AAX76
XX AAX76
XX AAX76
XX AAX76
XX Modu
KW Inhi
KW OB-C
KW Cadl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   are: (1) methods for alleviating neuropathic pain or inhibiting the C onset of neuropathic pain, comprising administering a prosaposin receptor agonist; (2) inhibiting sensory or motor neuropathy, comprising C contacting neuronal cells with a composition comprising a prosaposin cell or inhibiting neural cell death, promoting myelination, or inhibiting CC demyelination comprising contacting neuronal cells with a composition comprising a prosaposin receptor agonist which has 14-50 amino acids and CC comprises the sequence of a propsaposin derived protein. The processes CC may be used for treatment of neuropathic pain resulting from peripharal CC stretch, incomplete nerve transsection, mononeuropathy or polyneuropathy) CC thalamus or the cortex. The receptor agonists do not cause undesirable CC side effects. The present sequence represents a prosaposin receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
11-NOV-1999
                                                                                   W09957149-A2
                                                                                                                                                                  Disulfide-bond
                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                     cadherin-12; cadherin-14; cadherin-15; T-cadherin; PB-cadherin; cadherin; cadherin; related neuronal receptor; LI-cadherin; protocadherin; desmocollin; calcium binding; cancer; tumour; obesi; rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modulation; nonclassical cadherin mediated cell adhesion; CAR; inhibition; cadherin extracellular domain; cell adhesion recognition; OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-7; cadherin-8; cadh
                                                                                                                                                                                                                                                                                                                                                                                                                        neurological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cadherin-8 cell adhesion recognition cyclic peptide SEQ ID NO:1594.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY61736 standard; Peptide; 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Use of prosaposin receptor agonists - for alleviating neuropathic pain, inhibiting sensory or motor neuropathy, or inhibiting neural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 13; Page 19; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         O'Brien JS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1998-495790/42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 EHCNFNDVTT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 ehcslnenit 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention relates to prosaposin receptor agonists. Also claimed: (1) methods for alleviating neuropathic pain or inhibiting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A
                                                                                                                                                              Location/Qualifiers
1..8
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                                                                                                                                                                                                                                                                                                                                                                                                               cyclic.
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Pred. No. 1.3e+02;
Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                        sclerosis; diabetes; metastasis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           obesity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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CC inhibiting adhesion of nonclassical-cadherin expressing cells in a CC enhancing delivery of a drug through the skin of a mammal, enhancing delivery of a drug through the skin of a mammal, cancer in CC anancing delivery of a drug to a tumour in a mammal, treating cancer in CC angiogenesis in a mammal, inhibiting metastasis of a cancer in a mammal, treating cancer in CC angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-control of the control of
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         recognition (CAR) sequence. The MAs can be nonclassical cadherin-mediated functions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes cadherin modulating agents comprising peptides which comprise a nonclassical cadherin recognition (CAR) sequence. The MAS can be used for modulating the comprise of the compr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-MAY-1998;
06-NOV-1998;
20-JAN-1999;
08-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 42; Page 176; 252pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New cadherin modulating agents, used for modulating nonclassical cadherin-mediated functions for treating e.g. cancers, obesity, rheumatoid arthritis, multiple sclerosis, diabetes or a neurological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-MAY-1999;
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8 AA;
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98US-0187859.
99US-0234395.
99US-0264516.
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AAW43797
                                                                                                                                                    Db
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                                                                                                                                                                        Query Match
Best Local Similarity
Fighter 5; Conserv:
                      Human leukocyte antigen; HLA; vaccine; bacterial infection; viral;
cytotoxic T-cell; CTL; immunogenic peptide; cancer.
                                                Specific human leukocyte antigen binding peptide
                                                                       20-APR-1998
                                                                                          AAW43797;
                                                                                                     AAW43797 standard; peptide; 9
                                                                                                                                                                 4 CNFNDVT 10
                                                                                                                                                1 cqindvt 7
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                                                                                                                                                                                Conservative
                                                                     (first entry)
                                                                                                                                                                                         31.2%;
71.4%;
                                                                                                                                                                                         .48;
                                                                                                                                                                                0;
                                                                                                                                                                                        Score 30;
Pred. No.
                                                                                                                                                                              Mismatches
                                                                                                                                                                           Db _
4.3e+05;
2;
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Haemophilus influenzae

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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents a specific example of an immunogenic peptide which was used in a new method of inducing a cytotoxic T cell (CTL) response against a preselected antigen in a parient. The method comprises contacting CTLs from the patient with the immunogenic peptide (containing defined motifs) which binds one of the four HLA MHC products HLA-A3.2, HLA-A1, HLA-A1 or HLA-A24.1, the peptide having a dissociation constant (Kd) of less than 5 x 10-7 M. Immunogens are viral, e.g human immunodeficiency virus type I (HIV-1), hepatitis B virus (HBV) and
                                                                                                                                                                                                                                                                                   inhibition; cadherin extracellular domain; cell adhesion recognition; OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12; cadherin-14; cadherin-15; T-cadherin; PB-cadherin; cadherin related neuronal receptor; LI-cadherin; protocadherin; desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Specific human leukocyte antigen for the treatment and prevention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-MAR-1997;
21-MAR-1996;
                           WO9957149-A2
                                                                             Disulfide-bond
                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                               rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                           Modulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cadherin-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY61739 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hepatitis C virus (HCV) or cancer antigens and are used in vaccines for
the prevention and treatment of viral infection and cancer. The
immunogens may be administered to the patient as a nucleic acid encodin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Page 37; 49pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cell adhesion recognition cyclic peptide SEQ ID NO:1597.
                                                                                                                                                                                                                                                                                                                                                                                                                           nonclassical cadherin mediated cell adhesion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (gene vaccine).
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96US-0013833
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                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide;
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Pred. No. 4.
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of e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 18;
4.3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptide -
bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                              CAR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 blood vessel regression in a mammal, enhancing drug delivery to the central nervous system, treating a demyelinating neurological disease, increasing vasopermeability in a mammal, enhancing adhesion of nonclassical cadherin-expressing cells, inhibiting synaptic stability in a mammal, or preventing pregnancy in a mammal. They can also be used for e.g. enhancing or directing neurite outgrowth, facilitating wound healing of reducing scar tissue, or enhancing adhesion of foreign tissue in a mammal. They can also be used for treating e.g. psoriasis, arthritis, age-related macular degeneration, multiple sclerosis and diabetes. The products can also be used for detection and diagnosis and in bioreactors. AAY60592 to AAY6463 and AAX33183 to AAX33186 represent section and AAY64573 to AAY64643 and AAX33185 to AAX33186 represent
                             B cell; toxin; antigen specific; antibody mediated disease; virucide; immunosuppressive; antiinflammatory; antiallergic; antidiabetic; thyromimetic; antithyroid; vasotropic; cardiant; antiulcer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-
expressing cell, preventing or treating obesity in a mammal, stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           enhancing delivery of a drug to a tumour in a mammal, treating cancer in a mammal, inhibiting
               neuroprotective; antirheumatic;
                                                                                                                                 13-AUG-2001
                                                                                                                                                                AAB97334;
                                                                                                                                                                                                  AAB97334 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inhibiting adhesion of nonclassical-cadherin expressing cells in a mammal, enhancing delivery of a drug through the skin of a mammal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               recognition (CAR) sequence. The MAs can be used for modulat nonclassical cadherin-mediated functions. They can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes cadherin modulating agents comprising peptides which comprise a nonclassical cadherin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 42; Page 176; 252pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rheumatoid arthritis, multiple sclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New cadherin modulating agents, used for modulating nonclassical cadherin mediated functions for treating e.g. cancers, obesity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Blaschuk OW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-MAR-1999;
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20-JAN-1999;
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                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                               (first entry)
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98US-0187859.
99US-0234395.
99US-0264516.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the exemplification of the present invention
                                                                                                 domain
                                                                                                                                                                                                                                                                                                                                                                      31.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Byers
                                                                                                epitope peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The MAs can be used for modulating
                                                                                                                                                                                                  12
                                                                                                                                                                                                                                                                                                                                                      0,
                                                                                                                                                                                                                                                                                                                                                                      Score 30; DB 21;
Pred. No. 4.3e+05;
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                 antiarthritic;
                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diabetes or a neurological
                                                                                                                                                                                                                                                                                                                                                        2
                 dermatological;
                                                                                                                                                                                                                                                                                                                                                                                        Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MA)
cell adhesion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for e.g.
                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             stimulating
                                                                                                                                                                                                                                                                                                                                                      Gaps
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0

ophthalmological; nephrotropic; allergy;

autoimmune

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RESULT 1
AAW41168
ID AAW4
XX ,
AC AAW4
XX
                                                                                                                                                                                                                         immunosuppressive; antiinflammatory; antiallergic; virucide; antidiabetic; thyromimetic; antithyroid; vasotroplo; cardiant; antiulcer; conditant; antivological; cardiant; antivological; cophthalmological; and nephrotropic activity. The toxin is particularly mediated disease condition, where the antigen specific antibody is completed by an antigen-reactive B cell population present in a host. The coxin is useful for treating allergies, viral disease conditions, and complete commune disorders. Also treated are skin diseases; autoimmune disorders. Also treated are skin diseases; autoimmune communopathies; vasculitic syndromes; cardiovascular diseases; collagen vascular diseases; renal diseases; pulmonary diseases; collagen vascular diseases; renal diseases; pulmonary diseases; collapha 3 domain epitope peptide. An antibody response to this antigen is using the toxin of the invention.
                                                                                                                                                       Query Match
Best Local S
Matches 5
           AAW41168;
                             AAW41168 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention relates to a B cell clonal toxin. The toxin is made from two moieties, the first causes the toxin to be internalised by a B cell, and the second is a biologically acceptable toxin. The invention includes a method for inactivating/killing an antigen specific B cell. A target B cell is contacted with an effective amount of a B cell clonal characterised by the presence of an unwanted or deleterious immune response, e.g. in the treatment of antigen specific antibody mediated disease conditions. Use of the B cell clonal toxin can result in
                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B cell clonal toxin useful for treating autoimmune disorders such Grave's disease, myocardial infarction, Crohn's disease, multiple sclerosis, comprises a group that causes toxin to be internalized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 35; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-316435/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chaplin JW,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BIOM-) INST APPLIED BIOMEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-OCT-2000; 2000WO-US28157.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            skin diseases; autoimmune endocrinopathy; vasculitic syndrome; cardiovascular disease; immunohaematologic disorder; neurologic disease; gastrointestinal disease; collagen vascular disease; renal disease; pulmonary disease; infertility disorder; collagen IV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W0200132853-A1
                                                                                                      -
                                                                                                                            4 CNFNDV 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Goodpasture syndrome.
                                                                                                    cnvndv
                                                                                                                                                       Similarity 5; Conserv
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                                                                                                   6
                                                                                                                                                    Conservative
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                                                                                                                                                               31.2%;
83.3%;
                              15
                                                                                                                                             Score 30; DB 22;
Pred. No. 1.9e+02;
0; Mismatches 1
                              A
                                                                                                                                                                        Length 12;
                                                                                                                                             Indels
                                                                                                                                            0;
                                                                                                                                         Gaps
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Query Match
Best Local s
Matches 5
       11-OCT-1996;
29-MAY-1996;
                                           27-NOV-1996;
                                                                     04-DEC-1997.
                                                                                             W09745000-A1
                                                                                                                                   Synthetic
                                                                                                                                                       MRT; transgenic plant;
                                                                                                                                                                             Metal-regulated transporter epitope
                                                                                                                     Arabidopsis thaliana
                                                                                                                                                                                                           30-JUL-1998
                                                                                                                                                                                                                                    AAW41167;
                                                                                                                                                                                                                                                       AAW41167 standard; Protein; 16
                                                                                                                                                                                                                                                                                                                                                                                                                                               The metal regulated transporter epitope spans amino acids 162 through 184 of IRT1 (AAV12763). The peptide was used as an antigen to raise polyclonal antibodies. These antibodies recognize a protein of approximately 33KDa which is only present in iron starved plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel
DNA -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 16; Page 73; 144pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-032230/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eide DJ, Guerinot ML;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pollutants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (DART-) DARTMOUTH COLLEGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-OCT-1996;
29-MAY-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Metal-regulated transporter epitope.
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                                                                                                                                                                                                                                                                                                                                            7 NDVTTRLRENE 17
                                                                                                                                                                                                                                                                                                                       ndvtlpikedd 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    l A. thaliana metal-regulated transporter proteins and related for generating transgenic plants useful for removing utants from soil or providing nutrient to patients suffering metal-deficiency disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transgenic plant; pollution; metal-deficiency
                                                                                                                                                                                                                                                                                                                                                                        Similarity 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                    15 AA;
                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                      Conservative
      96CA-2187728
96US-0018578
                                          96WO-US19065
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96US-0018578
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                                                                                                                                                                                                                                                                                                                                                                                31.2%;
                                                                                                                                                  pollution; metal-deficiency.
                                                                                                                                                                                                                                                                                                                                                                   Score 30; DB
Pred. No. 2.3e
4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                            DB 15,
2.3e+02;
2;
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RESULT :
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Best Local S
Matches 5
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                    This peptide is an example of a peptide which binds to a human leucocyte antigen HLA-DQ4 molecule. The peptide was isolated from a phagemid combinatorial library comprising the sequence AAVO5953, by screening with an HLA-DQ4 molecule. The peptide is used for the treatment of autoimmune disease, or especially for treatment of viral diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 39;
                                                                                                                                                                                                                                                                                                                    autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                     Human leucocyte antigen DQ4 binding peptide #366
                                                                                                                                                                                                                                                                                                                                                                                                                       AAW49475 standard; peptide; 9 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eide
                                                                                                                HLA-binding oligopeptide and an immuno:regulator contg
the treatment of auto:immune disease
                                                                                                                                                                                                                                                                      JP08151396-A
                                                                                                                                                                                                                                                                                                                                                                             05-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                   AAW49475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184 of IRT1 (AAV12763). The polyclonal antibodies. These
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pollutants
Sequence
                                                                                          Claim
                                                                                                                                                   WPI; 1996-329479/33
                                                                                                                                                                         (TEIJ ) TEIJIN
                                                                                                                                                                                                 28-NOV-1994;
                                                                                                                                                                                                                        28-NOV-1994;
                                                                                                                                                                                                                                                11-JUN-1996
                                                                                                                                                                                                                                                                                                                              Human leucocyte antigen; HLA-DQ4; combinatorial library;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity les 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               metal regulated transporter epitope spans amino acids 162 through of IRT1 (AAV12763). The peptide was used as an antigen to raise yclonal antibodies. These antibodies recognize a protein of roximately 33KDa which is only present in iron starved plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A. thaliana metal-regulated transporter proteins and related for generating transgenic plants useful for removing utants from soil or providing nutrient to patients suffering metal-deficiency disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ndvtlpikedd 13
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                                                                                          4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DARTMOUTH COLLEGE.
UNIV MINNESOTA.
                                                                                        Page 43; 61pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page 105; 144pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Guerinot ML;
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9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
AA
                                                                                                                                                                                                                                                                                                                                                                             (first
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                                                                                                                                                                         LTD
                                                                                                                                                                                                94JP-0292657
                                                                                                                                                                                                                        94JP-0292657
                                                                                                                                                                                                                                                                                                                    chronic articular rheumatism
                                                                                                                                                                                                                                                                                                                                                                           entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 19;
2.5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 16;
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                                                                                                                            used
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Query Match

30 . 28;

Score

29;

DВ 17;

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RESULT 1
AAR71732
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B
                                                                 The merosin protein has an apparent mol. wt. of about 800 kD and is composed of four polypeptides with molecular weights of 300, 200, 200 and 80 kD. The 300 kD polypeptide is joined to the 200 kD polypeptides by disulphide bonds and the 300 and 80 kD polypeptides comprise the major subunit protein given in AAR71729. Merosin is found in placenta, compared to the 200 kD polypeptides of the major subunit protein given in AAR71729. Merosin is found in placenta, compared to the 200 kD polypeptides comprise the complexes, amoung other tissues. The 380-400 major merosin subunit also yields a 65 kD subunit. The 380-400 merosin subunit has been designated merosin polypeptide, merosin subunit, M chain or laminin M chain. These peptides may be used as antigens to raise anti-merosin antibodies. These antibodies may be used in the detection of merosin, as the absence of merosin in a tumour sample indicates malignancy. Contacting a compared to contacting inhibitors of neurite outgrowth, thereby also promoting the outgrowth. Merosin also promotes cell attachment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local
Matches
                                                                                                                                                                                                                                                                                                                                       the human laminin A chain. Mature human merosin is 30 amino acids larger than the human laminin A chain. Similarly to all laminin chains, the merosin protein has distinct domains which are predicted to have globular regions, cysteine-rich rod-like regions and helical structures. The merosin protein has an apparent mol. wt. of about 800 kD and is
                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequences given in AAR71731-32 represent peptides derived from the human 380-400 kD merosin major subunit protein. Merosin is an isoform of laminin and shows structural and sequence similarity to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; 380-400 kD; merosin; major subunit; placenta; straited muscle; peripheral nerve; trophoblast; Schwann cell neoplasm; 65 kD subunit; peripheral nerve; trophoblast; Schwann cell neoplasm; 65 kD subunit; merosin polypeptide; merosin subunit; M chain; 80 kD subunit; merosin polypeptide; merosin subunit; M chain; laminin M chain; antigen; antibody; detection; tumour; malignancy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tumour malignancy, promoti
promoting cell attachment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New merosin fragments, corresp. DNA and antibodies - tumour malignancy, promoting or inhibiting neurite gr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Engvall E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-SEP-1993;
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                                                       The merosin gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (LJOL-) LA JOLLA CANCER RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14
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hcnin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Page 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Leivo I;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neurite growth
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                                                                                                           polypeptide
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RESULT 1
AAB36546
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Best Local S
Matches 6
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Best Local Similarity 38.00,
Watches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δÃ
   AAB36546 standard; Peptide;
                                                                                                                                                                                    The present invention relates to two kinds of DNA sequences of coded human serum albumin (HSA), i.e. design of structure-modified gene segment of HSA and artificial total synthesis and a production process for large-scale production of genetic recombinant HSA by using methanol, yeast and engineering bacterium, and discovers that the structure-modified gene can greatly increase the expression quantity obtain high-level expression under the drive of promoter induced by methanol, and make the HSA expression product secrete into the fermenting liquor culture medium, and provide reliable test data for present sequence is given in the exemplification of the present
                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                   Disclosure;
                                                                                                                                                                                                                                                                                                                                                             Novel methods for chemical synthesis, expression and recombinant protein production for human serum albumin reformed gene -
                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-673206/66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                (MAOJ-) MAOJI BIOLOGICAL ENG SCI & TECH CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-MAR-1999;
                               16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CN1266099-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human serum albumin; HSA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human serum albumin (HSA) related (Venezia) peptide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-MAR-2001 (first entry)
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                                                                 Н
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                                                                                 2 EHCNFNDVTTRLRENE 17
                                                           etcfaeeptmrirerk 16
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                                                                                                        Similarity 37.5
6; Conservative
                                                                                                                                                                   16
                                                                                                                                                                                                                                                                                                                                               Fig 2; 85pp; Chinese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99CN-0102745.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99CN-0102745
                                                                                                                   30.2%;
37.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30.2%;
    16
                                                                                                   Score 29; DB 21; I
Pred. No. 3.6e+02;
3; Mismatches 7;
    A
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Pred. No. 3.1e+02;
2; Mismatches 6
                                                                                                                       Length 16
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                                                                                                   Indels
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Best Local :
     Disulfide-bond
                                                      Misc-difference
                                                                                                                             Synthetic
                                                                                                                                                                            asthenia;
                                                                                                                                                                                                    Hexapeptide #5 with learning response improvement properties
                                                                                                                                                                                                                                                                          01-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                 AAP20158 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to two kinds of DNA sequences of coded human serum albumin (HSA), i.e. design of structure-modified gene segment of HSA and artificial total synthesis and a production process for large-scale production of genetic recombinant HSA by using methanol, yeast and engineering bacterium, and discovers that the of HSA. The production process can make the expression quantity obtain high-level expression under the drive of promoter induced by fermenting liquor culture medium, and provide reliable test data for present sequence is given in the exemplification of gene engineering HSA. The invention
                                                                                                                                                                                                                                                                                                                            AAP20158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 2; 85pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel methods for the chemical synthesis, expression and recombinant protein production for human serum albumin reformed gene -
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nes 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MAOJ-) MAOJI BIOLOGICAL ENG
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                                                                                                                                                                                                                                                                                                                                                                                                                               17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 EHCNFNDVTTRLRENE 17
                                                                                                                                                                       memory loss;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16
                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ÃĀ;
/note= "D-form residue"
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                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30.2%;
37.5%;
                                                                                                                                                       learning; senility; metal complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 29;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 21; Le. . 3.6e+02; 7;
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Best Local S
Matches 4
                                                                                                                                                diabetes mellitus type II; microtubule associated protein; Tau; Big Tau; ubiquitin B; apolipoprotein E; MAP2; neurofilament-T; neurofilament-M; neurofilament-T; presentiln II; cellular tumour antigen; glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-I; bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          properties: it retards 1088 of response and aids attentiveness and conditioned avoidance response and aids attentiveness and memory. The peptide can be used in the treatment of memory failure, memory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hexa:peptide(s) used to treat asthenia, cerebral vascular troubles etc - include Cys-Ala-Ala-Phe-D-Lys-Cys, Cys-Ala-Ala-Cys-D-Lys-Phe and Cys-Glu-His-Cys-D-Lys-Phe, their
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EP52028-A.
10-APR-1997;
                        02-APR-1998;
                                                 15-OCT-1998
                                                                          W09845322-A2
                                                                                                                                                                                                               Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal; Huntington's disease; multiple sclerosis; alcoholic liver disease;
                                                                                                                                                                                                                                                      Human; beta-amyloid precursor protein; beta-APP; diagnosis;
                                                                                                                                                                                                                                                                               Human microtubule associated protein 2 mutant fragment 152
                                                                                                                                                                                                                                                                                                          22-JUL-1999
                                                                                                                                                                                                                                                                                                                                   AAY20456
                                                                                                                                                                                                                                                                                                                                                             AAY20456 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  di:sulphide(s) and metal complexes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gasc JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-OCT-1980;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-OCT-1981;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-MAY-1982.
                                                                                                Homo sapiens
                                                                                                                                                                                                                                           frameshift mutation;
                                                                                                                                                                                                                                                                                                                                                                                      18
                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 EHCNF 6
                                                                                                                                                                                                                                                                                                                                                                                                                          2 ehckf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  peptide is specifically claimed and has the following erties: it retards loss of learned responses, it retar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Page 16; 20pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cerebral
See also
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                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA;
                                                                                                                                     group protein-C; neuroendocrine specific protein A
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97US-0043163
                        98WO-IB00705
                                                                                                                                                                                                                                                                                                                                                             Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vascular disturbances and AAP20155-7 and AAP20407.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29.2%;
                                                                                                                                                                                                                                           age-related disease; neurodegenerative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hospital M,
                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 28; DB
Pred. No. 4.3e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 3;
4.3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                      cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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intramolecular

Mycoplasma genitalium; complementary peptide; protein-protein interaction; drug design; drug design; interaction; drug design; drug des

intermolecular;

Mycoplasma genitalium intermolecular complementary peptide,

QES

ID

387.

22-OCT-2001 AAM43078;

(first entry)

13-DEC-1999;

13-DEC-2000; 2000WO-GB04778

14-JUN-2001 WO200142278-A2 Mycoplasma genitalium AAM43078

AAM43078 standard; Peptide;

10

RESULT

19

Вþ Qy

1 fhhcsan

0

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Matches
                                                   Query Match
Best Local
                                                                                                                                                    disease, Down's syndrome, myotonic dystrophy, Huntington's disease, multiple sclerosis, alcoholic liver disease, diabetes mellitus type II and many others listed) or susceptibility to these disorders. The method allows a definitive diagnosis of Alzheimer's disease in living patients, at an early stage. It is based on the observation that disease may be caused by mutations in RNA rather than DNA. The invention describes the used of neuronal system RNA molecules, specifically proteins including beta-amyloid precursor protein (beta-ApP), the microtubule associated protein 2 (MAP2), neurofilament-L, neurofilament-M, neurofilament-F, presenilin I, presenilin I, gilal fibrillary acidic protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma 2 (bcl-2) proto-oncogene, semaphorin III, HUPF-1, high mobbility group protein-C (HMGP-C) and neuroendocrine specific protein A.
                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes a novel method for the diagnosis of a caused by, or associated with, an RNA molecule that has a fram mutation. The method is used to diagnose age-related diseases, cancer and a wide range of neurodegenerative disorders (e.g. A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Diagnosing disease by detecting frameshift mutations in RNA or corresponding protein mutations - used to diagnose cancer and neurological diseases, particularly Alzheimer's disease, and also for treatment and prevention with specific ribozymes or wild-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYUT-)
(ROYA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-609901/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Burbach JPH,
                                                                                                                        Sequence
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1 FEHCNEN 7
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ROYAL NETHERLANDS ACAD ARTS
UNIV ROTTERDAM ERASMUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAX75757
                                     4.
                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Figure
                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6;
                                                   29.2%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                258pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Van Leeuwen FW
                               Score 28; DB 19;
Pred. No. 4.3e+05;
1; Mismatches 2
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                                     2
                                                                Length 9;
                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                of a disease
frameshift
                                     0;
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Alzheimer's
                                     Gaps
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RESULT 2
AAY57800
ID AAY5
XX AAY5
AC AAY5
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KW Creh
KW Creh
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KW Creh
KW Vire
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Best Local Similarity 55.6
5; Conservative
WPI; 2000-072620/06
                                                           Ö'Connor MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                        Transcriptional adapter motif; TRAM; TRAM interaction motif; TRIM; creb binding protein; transcriptional regulation; cytostatic; antiviral; cell cycle inhibitor; viral transcription inhibitor; cancer; tumour; viral disease; viral infection; cell cycle; apoptosis; growth arrest.
                                                                                                                   (MOLE-) INST
                                                                                                                                                                         26-MAY-1998;
05-JAN-1999;
                                                                                                                                                                                                                                                         26-MAY-1999;
                                                                                                                                                                                                                                                                                                              02-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                       WO9961608-A2
                                                                                                                                                                                                                                                                                                                                                                                                                            Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRAM-interaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-MAR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY57800 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is one of a large number of complementary peptide ligands generated from Mycoplasma genitalium genome sequences. These specific complementary peptides interact with their relevant target antagonising complementary peptides interact with their relevant target antagonising or agonising specific interaction of a protein with another protein or receptor and are thus useful as reagents and drugs, and as lead ligands to facilitate drug design and development. They configuration of high-throughput screens, as a starting point for the medicinal chemistry manipulation, for peptide mimetics and as facilitates understanding of protein-protein interactions. The method allows for analysis and acquisition of peptide sequences facilitates understanding of protein-protein interactions. The method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sampling problems. The set of complementary peptides includes intermolecular (between proteins) and intermolecular (within a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    facilitates understanding of protein protein interactions. The method allows for analysis of an entire database at a time, thus overcoming sampling problems. The set of complementary peptides includes both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 2; Page 103; 161pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PROT-) PROTEOM LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 FNDVTTRLR 14
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                                                                                                       MOLECULAR & CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                     Zimmermann H;
                                                                                                                                                                98GB-0011303.
99GB-0000157.
                                                                                                                                                                                                                                                   99WO-GB01668
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29.2%;
                                                                                                          BIOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 28;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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tches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
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Best Local
Polypeptide exhibiting lepidoptera allostatin like activity inhibiting juvenile hormone synthesis, used as insecticide a insect population control agent
                                                             WPI; 1991-104135/15
                                                                                         Kramer SJ,
                                                                                                                    (SANO ) SANDOZ
                                                                                                                                             02-OCT-1989;
                                                                                                                                                                     28-SEP-1990;
                                                                                                                                                                                                  10-APR-1991.
                                                                                                                                                                                                                           EP421935-A.
                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                     LAS; juvenile
                                                                                                                                                                                                                                                                                                                                        Lepidoptera allostatin polypeptide analogue
                                                                                                                                                                                                                                                                                                                                                                        11-JUN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                        AAR11465 standard; peptide; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              useful for preparing a pharmaceutical composition and for disrupting an interaction between TRAM sequence and TRIM sequence in vitro, thereby cells especially cancer cell. Compounds which disrupt interaction between TRIM/TRAM containing polypeptides can be used therapeutically to prevent or treat viral diseases and tumours. The polypeptides reduce susceptibility of cells to viral infection and regulate cell cycle antibodies against the TRIM or TRAM sequences. HPV types associated with high risk or low risk of cervical cancer can be distinguished (CBP) TRAM sequence. The present sequence represents a TRIM from an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                     AAR11465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes a polypeptide comprising a transcriptional adaptor motif (TRAM) or a TRAM-interaction motif (TRIM) (I). (I) can be used for identifying compounds (II) comprising a polypeptide capable of disrupting an interaction between a TRAM sequence and/or a TRIM sequence. Polypeptides which bind to a TRAM sequence or a determining if the polypeptide interacts with (I). Compound (II) is marked in the polypeptide interacts with (I).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel polypeptides cells useful for treating viral disease and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Fig 2; 73pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                        Miller CA,
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                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                               hormone; insecticide
                                                                                                                                           89US-0416097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA;
                                                                                                                                                                    90EP-0810745
                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                              /note= "pyroglutamine"
                                                                                                                                                                                                                                                               /label= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29.2%;
57.1%;
                                                                                    Schooley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 28; DB 21;
Pred. No. 4.2e+02;
2; Mismatches 1
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                                                                                     DA,
                                                                                  Toschi AG
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RESULT :
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Best Local
                        The present sequence represents a mimotope which functionally mimics a binding site for a monoclonal antibody (MAb) which recognises an epitope within the human platelet glycoprotein (gp) Ib/IX complex. More specifically the MAb is SZ-2. The mimotope peptide can be used for raising antibodies, as probes to search for anti-mimotopes and to neutralise the inhibitory activity of those antibodies which recognise the epitope which is mimicked by the peptide. Anti-mimotopes can be used to modulate the adhesion, aggregation or agglutination of platelets by affecting von Willebrand factor interaction with the platelets through the gp Ib/IX receptor, e.g. as an anti-thrombotic drug which inhibits the ristocetin induced aggregation of platelets.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This lepidoptera allostatin (LAS) polypeptide analogue is an example of a highly generic polypeptide sequence. It exhibits LAS-like activity and inhibits juvenile hormone (JH)-I, -II and -III activity in lepidoptera. It is used as an insecticide or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human platelet glycoprotein Ib/IX complex epitope; mimotope; probe; monoclonal antibody SZ-2; anti mimotope; binding site; antibody; platelet adhesion; aggregation; agglutination; von Willebrand factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim
                                                                                                                                                                                                                                  Peptide which mimics human platelet glycoprotein Ib/IX complex epitope - also anti-mimotope molecule capable of binding to the peptide and useful to modulate platelet adhesion, aggregation or agglutination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW32738 standard;
                                                                                                                                                                                                         Claim
                                                                                                                                                                                                                                                                                                                                       Lyle VA,
                                                                                                                                                                                                                                                                                                                                                                                                  13-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9718236-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human platelet
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW32738;
Sequence
                                                                                                                                                                                                                                                                                                           WPI; 1997-289227/26
                                                                                                                                                                                                                                                                                                                                                                    (UYNY ) UNIV NEW YORK STATE RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                              08-NOV-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           thrombotic drug; ristocetin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6;
                                                                                                                                                                                                     8; Page 99; 115pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          population control agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                page
                                                                                                                                                                                                                                                                                                                                        Miller JL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,
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                                                                                                                                                                                                                                                                                                                                                                                                 95US-0556597.
                                                                                                                                                                                                                                                                                                                                                                                                                              96WO-US17882
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peptide; 10 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ib/IX complex epitope mimotope
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4.8e+02;
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                                                                                                                                                                                                                                                aggregation or
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Best Local S
Matches 6
Query Match
Best Local
                                                                                       This invention describes novel polypeptides of formula RaXRb where X = C(=0), HNC(=5), HNC(=0)CH2 or CH2; Ra = fluorescein, rhodamine, Texas red, a 'Bodipy' (RTM), 'Cascade Blue' (RTM), coumarin, phycoerithryn, eosin or rosamine; and Rb = a polypeptide of 29 or 30 amino acids selected from 26 sequences given in the specification. Such peptides are useful for the treatment of hypothalamic pituitary dwarfism, burns, osteoporosis, renal failure, non-union bone fracture, acute or chronic debilitating illness or infection, wounds, lactation failure, infertility in women, cachexia in cancer patients, anabolic and/or catabolic problems, T-cell immunodeficiencies, neurodegenerative conditions or growth hormone releasing factor (GRF) receptor-dependent tumours and for reduction of the incidence of post-surgical problems and as markers for GRF receptors.
                                                                                                                                                                                                                                                                                                                                                               New polypeptide derivatives are growth hormone releasing factor receptor agonists - useful for treatment of e.g. dwarfism, burns, osteoporosis, renal failure, infections, infertility, cachexia and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Growth hormone releasing factor; GRF; human; treatment; osteoporosis; hypothalamic pituitary dwarfism; burn; renal failure; infection; wound; non-union bone fracture; lactation failure; female infertility; cachexia; cancer; anabolic; catabolic; T-cell immunodeficiency; tumour; marker; neurodegenerative condition; post-surgery.
                                                                                                                                                                                                                                                                                                                    Disclosure; Column 39-40; 26pp; English.
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                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                    FURIOUIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-SEP-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW93135 standard; peptide; 12
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nes 6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23
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1 khcs---ihtrlr 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MONTREAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                              AA;
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94US-0312244.
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28.1%;
50.0%;
Score 27; I
Pred. No. 5.
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Pred. No. 3
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DB 20;
5.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 18;
.8e+02;
              20;
              Length 12;
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cc ingredient which specifically and selectively binds to a natural cylorest provided by the provided control of the provided by the provided by the provided control of the provided by the p
                                                              treating diseases associated with hyaluronic acid, such as stroke and in combination with chemotherapeutic agents. They can be used to treat with glioblastoma multiforme. The peptides are also useful for treating ameliorating and/or preventing infectious diseases such as HTV mediates binding between the sperm annot the ocyte. The peptides a a contraceptive as HA better inhibition of glycosaminoglycan-mediated activity than larger, e.g., anti-CD44 antibodies, and are more specific than chemical
        inhibitors of glycosaminoglycans such as tunimycin and H7. are significantly smaller than other inhibitors of are significantly smaller than other inhibitors of are significantly smaller.
     glycos,aminoglycan-mediated activity such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 4; Page 26; 53pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel composition useful as inhibitor or enhancer of glycosaminoglycan-mediated processes, for treating or infections, inflammatory diseases and cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a novel composition comprising an active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Takashima A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-MAR-2000; 2000WO-US07813.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hyaluronic acid-binding peptide; glycosaminoglycan; autoimmune diseas HA-CD44 mediated immune cell migration inhibitor; inflammatory diseas leukocyte infiltration inhibitor; lupus erythematosus; rheumatoid arthritis; graft-versus host disease; infectious disease; hyaluronic acid associated disease; stroke; myocardial infarction; cancer; brain tumour; oedema; glioblastoma multiforme; HIV; contraceptive; phage display library peptide.
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Matches

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RESULT 25
AAP81811
ID AAP818
      Query Match
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                                                                Antigenic and immunogenic conjugates contg. the peptides and a kit to detect HIV-2 in biological fluids are new. The peptides are useful for in vitro diagnosis of HIV-2 infection and some of them can be used as components of immunogens and vaccines against HIV. Antibodies raised against them can be used for treatment of AIDS.
                                                     Sequence
                                                                                                                          New peptides which have immunological properties in common with those of the epitide skeleton of the envelope protein of HIV-2 and also have a peptide structure in common with that of SIV-1 glycoprotein are claimed.
                                                                                                                                                                                     Claim 12;
                                                                                                                                                                                                 New peptide(s) with immunological properties of HIV-2 envelope protein have the structure of simian immune deficiency virus proteins, useful in diagnosis and of vaccine components
                                                                                                                                                                                                                                                                               Alizon M, I
Tiollais P,
                                                                                                                                                                                                                                                                                                             (INSP ) INST PASTEUR (ALIZ/).
                                                                                                                                                                                                                                                                                                                                         14-APR-1987;
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                                                                                                                                                                                                                                                                                                                                                                                                             WO8805440-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence of peptide with immunological properties and HIV-2 and SIV.1 glycoproteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antigen;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 glycosaminoglycan, allowing for improved oral and and are more cost effective to produce. Sequences represent the hyaluronic acid- binding peptide of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunogen; vaccine; diagnostic; AIDS
                                                                                                                                                                                    Page 44;
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                                                                                                                                                                                                                                                                           Montagnier L, Gu, Chakrabarti L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 AA;
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DB 9;
6e+02;
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           Length 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       structure
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Search completed: April 2, 2002, 09:24:40 Job time: 109 sec

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Maximum Match 100%
Listing first 50 summaries
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Maximum DB seq length: 17
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Perfect score:
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1: /cgn2_6/ptodata/2/paa/Us

2: /cgn2_6/ptodata/2/paa/Us

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Gapop 10.0 , Gapext 0.5
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/cgn2_6/ptodata/2/paa/US06_COMB.pep:*
/cgn2_6/ptodata/2/paa/US07_COMB.pep:*
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/cgn2_6/ptodata/2/paa/US60_COMB.pep:*
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52.307 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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99-835-752-1 99-607-158-9 39-607-535-6 3-287-535-1 1594-08453-11 8-32-513-11 8-824-238-11 9-824-808-11
Ouery Match Length DB ID 44.8 15 22 US-09-69-752-1 34.4 15 6 US-08-287-535-6 33.3 16 1 PCT-US94-08453-11 33.3 16 12 US-08-824-2388-11 33.3 16 12 US-08-824-808-11 33.3 16 12 US-08-824-2388-11 33.3 16 12 US-08-824-2388-11 33.3 16 12 US-08-824-2388-11 33.3 16 17 US-08-824-808-11 33.3 17 1 PCT-US97-04143-16
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29,	16, 15, 15, 15, 15, 15, 15, 15, 15, 15, 15	4, 34, 34, 133, 133, 20, 20, 20, 12,	Sequence 16 Sequence 17 Sequence 18 Sequence 28 Sequence 28 Sequence 28 Sequence 28

ALIGNMENTS

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Query Match
Best Local Similarity
7; Conserve
                                                                                                                                        ; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-835-752-1
                                                                                                                                                                                                                                                                                                                                                           US-09-835-752-1
; Sequence 1, Application US/09835752
; GENERAL INFORMATION:
                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/835,752
CURRENT FILING DATE: 2001-04-16
PRIOR APPLICATION NUMBER: US 06/203,254
PRIOR FILING DATE: 2000-05-08
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                               APPLICANT: Halperin, Jose
TITLE OF INVENTION: Methods, Products and Treatments for Diabetes
FILE REFERENCE: H0498/7137(ERG)
   7
              1 FEHCNFND 8
FEHANFND 14
                                                              Conservative
                                                                             44.8%;
87.5%;
                                                              0;
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Pred. No.
                                                              Mismatches
                                                                             DB 22;
6.9;
                                                                                           Length 15;
                                                              Indels
                                                              0;
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US-08-287-535-6
                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM/PC or Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WOrdperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/287,53:
FILING DATE: Not Yet Assigned
CLASSIFICATION: 514
PRIOR APPLICATION: 514
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
TENUTUM: 15 MACTOR STATA:
INFORMATION FOR SEQ ID NO: 6:
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                                  Matches
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                                                   Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9, Application US/09607158
GENERAL INFORMATION:
APPLICANT: SARANAKA, MASAHIRO
APPLICANT: TANAKA, JUNYA
APPLICANT: SATO, KOHJI
APPLICANT: MORITA, FUNIO
APPLICANT: SADAMOTO, YASUTAKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-607-158-9
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 9
LENGTH: 17
TYPE: PRT
                                                                                                                       LENGTH: 15 Amino Acids
TYPE: Amino Acid
TOPOLOGY: Linear
MOLECULE TYPE: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/607,158
CURRENT FILING DATE: 2000-06-29
NUMBER OF SEQ ID NOS: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: SADAMOTO, YASUTAKA
TITLE OF INVENTION: CYTOPROTECTIVE AGENTS COMPRISING PROSAPOSIN-RELATED
TITLE OF INVENTION: PEPTIDES
FILE REFERENCE: 49960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Moe, Gregory R.
TITLE OF INVENTION: Conformationally-Stabilized Peptides
TITLE OF INVENTION: and Use Thereof As Immunogens
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Connolly and Hutz
                                Local Similarity les 5; Conserv
4 CNFNDVTTRLR 14
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60.0%;
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                      Score 33; DB Pred. No. 3e+0
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Pred. No. 53;
                                      DB 6;
3e+02;
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                   Indels
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RESULT 5
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Best Local Similarity
Thes 5; Conserve
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                                                                                                                                Sequence 11, Application US/08232513 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: ISTAELSEN, Ned A.
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: OBRITELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-850
TELEPHONE: (619) 235-0176
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYDE: maino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/08453
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 08/100.247
FILING DATE: 30-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Tersoles Nod Nod Name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCT-US94-08453-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 11, Application:
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive, Sixteenth Floor
                                                    TITLE OF INVENTION: Prosaposin and Cytokine-Derived Peptides TITLE OF INVENTION: as Therapeutic Agents
NUMBER OF SEQUENCES: 14
                                                                                                              APPLICANT: O'Brien, John S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      LUNCERISTICS:
16 amino acids
LIPE: amino acid
STRANDEDNESS: s:
TOPOLOGY:
OLEGULP
TPOCOULP
                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL: 1
ANTI-SENSE: NO
FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-POS/MS-DOS
Tolage #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                       2 EHCSLNENIT 11
                                                                                                                                                                                                                                                                      2 EHCNFNDVTT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 620 NC., CITY: Newport Beach
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Newport Beach
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                                                                                                                                                                                                                                                                                                       Conservative
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620 Newport Center Drive, Sixteenth Floor
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Pred. No. 4.8e+02;
2; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                           DB 1; Length 16;
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COMPUTER READABLE FORM:

92660

MEDIUM TYPE:

Floppy disk

COUNTRY:

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Query Match
Best Local Similarity
Thehas 5; Conserve
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; FRAGMENT TYPE:
US-08-232-513-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION: (619) 235-8550
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: spino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
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FILING DATE: 30-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: ISTAELSEN, Ned A.
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: OBRIEN.002
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE N
HYPOTHETICAL: N
                 ATTORNEY/AGENT INFORMATION:
NAME: Israelsen Ned A
                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/100,247
FILING DATE: 30-JUL-1993
                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive, Sixteenth Floor
                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Prosaposin and Cytokine-Derived Peptides TITLE OF INVENTION: as Therapeutic Agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: O'Brien,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                 CITY:
STATE:
                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                ZIP:
NAME: Israelsen, Ned A. REGISTRATION NUMBER: 29,655
                                                                                                              CLASSIFICATION: 530
                                                                                                                               APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                            COUNTRY:
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Pred. No. 4.8e+02;
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Query Match
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US-08-824-808-11
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US-08-824-808-11
                                                                                                        TELEPAX: (619) LOOK INFORMATION FOR SEQ ID NO: 1)
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
1.FNGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 11, Application US/08824808 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (619) 235-0176 INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 30-JUL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: OF TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: O'Brien, John S.
TITLE OF INVENTION: Prosaposin and Cytokine-Derived Peptides
TITLE OF INVENTION: as Therapeutic Agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: PO
HYPOTHETICAL: NO
ANTI-SENSE: NO
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TELECOMMUNICATION INFORMATION:
                            HYPOTHETICAL: I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                         MOLECULE TYPE:
             FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 620 Newport Beach
                                                                                                                                                                                                                                     NAME: Israelsen, Ned A REGISTRATION NUMBER: 29
                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/824,808 FILING DATE:
                                                                            TOPOLOGY:
                                                                                         STRANDEDNESS:
                                                                                                                                                                                      TELEPHONE:
                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
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Pred. No. 4.8e+02
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RESULT 8
US-09-017-259-11
Sequence 11, Application US/09017259
GENERAL INFORMATION:
APPLICANT: O'Brien, John S.
TITLE OF INVENTION: Prosaposin and Cytokine-Derived Pepti INVENTION: AS Therapeutic Agents
OUNBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear STREET: 620 Newport Center Drive, Sixteenth Floor
                                                                                   RESULT 9
PCT-US97-04143-16
                                                                                                                                                                                                                                                                                             ; ANTI-SENSE: NO; FRAGMENT TYPE: US-09-017-259-11
                                 Sequence 16, Application PC/TUS9704143

CENERAL INFORMATION: The Regents of the Univ.
                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSITICATION DATA:
PRIOR APPLICATION NOMBER: 08/824,238
APPLICATION NUMBER: 08/824,238
APPLICATION NUMBER: US 08/100,247
FILING DATE: 30-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned A.
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: 0BRIEN.002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEPAN: (619) 235-0176
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
          APPLICANT: The Regents of the University of California TITLE OF INVENTION: Methods of Alleviating Neuropathic Pain
                                                                                                                                                                                                                                                                                                                       MOLECULE
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOPTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
                                                                                                                                                                                                                                 Local
                                                                                                                                                                                2 EHCNFNDVTT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: UZIP: 92660
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les 5; Conserv
                                                                                                                                                  EHCSLNENIT 11
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                                                                                                                                                                                                                                                                                                                                     NO Peptide
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                                                                                                                                                                                                                                                                                                          internal
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Pred. No. 4
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Pred. No. 4.8e+02;
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4.8e+02;
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Best Local Similarity
Watches 5; Conserve
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      APPLICATION NUMBER: PCT/US97/04143
FILING DATE: 05-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph.D., Lisa A.
                                                                      APPLICATION NUMBER: 08/6
FILING DATE: 05-MAR-1996
PRIOR APPLICATION DATA:
                                                                                                                 APPLICATION NUMBER: US/0
FILING DATE: 11-SEP-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (619) 535-89 INFORMATION FOR SEQ ID NO:
                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: O'Brien, John S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                     STATE: CA
COUNTRY: US
ZIP: 92037
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: FP
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILLING CLASSIFICATION:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
NAME: 31,815
REGISTRATION
                                                                                                                                                                                                 COMPUTER: IBM CONTROL OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                  STREET: 4225 E:
CITY: La Jolla
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: US
NUMBER OF SEQUENCES: 2:
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/08928074
                                                                                                                                                                                                 IBM Compatible
SYSTEM: Windows95
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25_Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                    Diskette
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                                                                                                                                                                                                                                                                                                                                                                              METHODS FOR ALLEVIATING NEUROPATHIC PAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33.3%;
50.0%;
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                                                                                                    08/611,307
                                                                                                                                                  US/08/928,074
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Pred. No. 5
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Best Local Similarity
Thes 5; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence: Artificial; OTHER INFORMATION: Peptide Sequence (hEPO) US-08-928-074-16
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US-08-928-074-16
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                                                                                                                                                                                                                                                         Sequence 16, Application US/08928074B GENERAL INFORMATION:
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 16
LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local
                                                     APPLICANT: O'Brien, John S.
TITLE OF INVENTION: METHODS FOR ALLEVIATING NEUROPATHIC PAIN
FILE REPERINCE: 07256/024001
GURRENT APPLICATION NUMBER: US/08/928,074B
CURRENT FILING DATE: 1997-09-11
EARLIER APPLICATION NUMBER: 08/611,307
EARLIER FILING DATE: 1996-03-05
EARLIER APPLICATION NUMBER: PCT/US97/04143
EARLIER APPLICATION NUMBER: PCT/US97/04143
EARLIER FILING DATE: 1996-03-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EARLIER APPLICATION NUMBER: 08/611,307
EARLIER FILING DATE: 1996-03-05
EARLIER APPLICATION NUMBER: PCT/US97/04143
EARLIER FILING DATE: 1996-03-05
NUMBER OF SEQ ID NOS: 25
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TITLE OF INVENTION: METHODS FOR ALLEVIATING NEUROPATHIC PAIN FILE REFERENCE: 07256/024001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/08/928,074A CURRENT FILING DATE: 1997-09-11
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LENGTH: 17 amino acids
TYPE: amino acid
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
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Pred. No.
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Pred. No. 5.1e+02;
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; NAME/KEY: Peptide
; LOCATION: 1..17
; OTHER INFORMATION:
US-09-172-713-11
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                 Query Match
Best Local Similarity
Thes 5; Conserve
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                  FEATURE:
                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08
FILING DATE: 21-APR-1994
APPLICATION NUMBER: US 08
FILING DATE: 30-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
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                                                                                                                                                                                               TOPOLOGY:
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   2 EHCNFNDVTT 11
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4370 La Jolla Village Drive, Suite 700
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                               Conservative
                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                      (619)
                                                                                                                                                                              peptide
                                                                                                                                                                                                                                                                       535-8949
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50.0%;
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Pred. No.
                               2;
                                             Score 32; DB 15;
Pred. No. 5.1e+02;
                                Mismatches
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5.1e+02;
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RESULT 16
US-09-839-542-1594
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                                                                                                                                                                                                                            Query Match
Best Local Similarity
Thehes 5; Conserve
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; OTHER INFORMATION: Representative cyclic modulating agent based on OTHER INFORMATION: cadherin-8 cell adhesion recognition sequence US-09-187-859-1594
      Sequence 1594, Application US/09839542
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Symonds, James_Matthew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-187-859-1594; Sequence 1594, A
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Best Local Similarity
"~+~hes 5; Conserv
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1594, Application US/09187859A
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL TITLE REFERENCE: 100086.407C1
CURRENT APPLICATION NUMBER: US/09/187,859A
CURRENT FILLNG DATE: 1938-11-06
CURRENT FILLNG DATE: 1938-11-06
SOFTWARE: Patentin Ver. 2.0
SEO ID NO 1504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 1594
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US-09-187-859-1594
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GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Blaschuk, Orest W.
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL TITLE OF INVENTION: CADHERIN MEDIATED FUNCTIONS
CURRENT APPLICATION NUMBER: US/09/187,859
CURRENT APPLICATION NUMBER: US/09/187,859
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: Patentin Ver. 2.0

SOFTWARE: Patentin Ver. 2.0

LENGTHUM 1594
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ORGANISM: Artificial Sequence
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71.4%;
                                                                                                                                                                                                                                    Score 30; DB 15;
Pred. No. 2.9e+06;
0; Mismatches 2
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Pred. No. 2.9e+06;
Prematches 2;
                                                                                                                                                                                                                                                                       Length 8;
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; TOPOLOGY: 11; MOLECULE TYPE: US-08-821-739-1
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                                                                                                                                       CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,833
FILING DATE: 21-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-000
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-821-739-1
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; OTHER INFORMATION:
US-09-839-542-1594
                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Applicati
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/OCCURRENT FILING DATE: 2001-04-20 NUMBER OF SEQ ID NOS: 4052 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 1594 LENGTH: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Kubo, Ralph T.
APPLICANT: Grey, Howard M.
APPLICANT: Sette, Alessandro
APPLICANT: Celis, Esteban
TITLE OF INVENTION: HLA BINDIN
TITLE OF INVENTION: Uses
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Best Local :
                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS FILE REFERENCE: 100086.407D1
                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 149
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
                                          STRANDEDNESS:
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                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 20-MAR
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ZIP: 94111-3834
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CITY: San Francisco
STATE: California
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20-MAR-1997
                                           single
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Pred. No. 2.9e+06;
0; Mismatches 2;
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Best Local Similarity
""" hes 5; Conserv
                                                                                                                                          ; OTHER INFORMATION: Representative cyclic modulating agent based on ; OTHER INFORMATION: cadherin-8 cell adhesion recognition sequence US-09-187-859-1597
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/187,859
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 1597
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                                                                 Matches
                                                                                              Query Match
                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1597
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APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
                                                                                                                                                                                                                                                                                          APPLICANT: Blaschuk, Orest W.
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
FILE REFERENCE: 100086.407C1
CURRENT APPLICATION NUMBER: US/09/187,859A
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 4052
                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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CQINDVT 7
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                                                                                Score 30; DB 15;
Pred. No. 2.9e+06;
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                                                                 Mismatches
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2.9e+06;
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Query Match
Best Local Similarity
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LENGTH: 9
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APPLICANT: Symonds, James Matthew
APPLICANT: Gour, Barbara J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/839,542
CURRENT FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: Patentin Ver. 2.0
                                                                       TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Silveri, Jean M.
REGISTRATION NUMBER: 39,
                                 SEQUENCE CHARACTERISTICS: LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Metal-Regulated Transporters and Uses NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                            STREET: STREET: Massac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
TOPOLOGY:
                   TYPE:
                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/0 FILING DATE: 29-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
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linear
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Pred. No. 2.9e+06;
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MOLECULE TYPE: FRAGMENT TYPE:

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PCT-US96-19065-21

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RESULT 24
US-09-169-404-23
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US-60-300-614-28
; Sequence 28, Application US/60300614
; GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL POTASSIUM CHANNEL WITH HOMOLOGY TITLE OF INVENTION: AMYCDALA OF HUMAN BRAIN
; FILE REFERENCE: D0123 PSP1
                                                                                                                                                                                                                 ; ORGANISM: Homo sapiens US-60-300-614-28
Sequence 23, Application US/09169404
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Best Local Similarity
""" Conserve
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Sequence 28, Application US/60299378
Sequence 28, Application US/60299378
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLECTIDE ENCODING A NOVEL POTASSIUM CHANNEL WITH HOMOLOGY TITLE OF INVENTION: AMYGDALA OF HUMAN BRAIN
FILE REFERENCE: D0123
CURRENT APPLICATION NUMBER: US/60/299,378
CURRENT APPLICATION UMBER: US/60/299,378
CURRENT FILLE DATE: 2001-06-19
SEQ ID NO 28
SEQ ID NO 28
LENGTH: 13
                                                                                                                                            Matches
                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                   SOFTWARE: PatentIn version 3.0
SEQ ID NO 28
LENCTH: 13
TYPE: PRT
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CURRENT FILLING DATE: 2001-06-25
NUMBER OF SEQ ID NOS: 52
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Best Local Similarity 45.5%;
Matches 5; Conservative
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                                                                                                                                                    30.2%;
57.1%;
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Pred. No. 1.2e+03;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 30; DB 1;
Pred. No. le+03;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2;
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RESULT 25
US-07-669-789-4
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Best Local Similarity
Matches 5; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-169-404-23
                                                                                                                                   Sequence 4, Application US/07669789
GENERAL INFORMATION:
APPLICANT: Liu, Chung-Cheng
TITLE OF INVENTION: Use of Purified Ubiquitin Hydrolase in Recovering Polypepti
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/125,077

FILING DATE: 22-SEP-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US PCT/US 94/10730

FILING DATE: 21-SEP-1994

PRIOR APPLICATION DATA:

APPLICATION UMBER: US 07/472,319

FILING DATE: 30-JAN-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/919,951

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO:
COMPUTER READABLE FORM:
                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
                                                           STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                     COUNTRY: US
                                                                                                    STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-D
SOFTWARE: PATENTIN Rel.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Engvall, Eva
APPLICANT: Leivo, Ilmo
TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin
TITLE OF INVENTION: Fragments and Uses Thereof
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                  1 CSIVDIDINGEEN 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE:
                                                                                                                                                                                                                                                                                                                                                                                        4 CNFNDVTTRLREN 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Campbell, Cathryn A REGISTRATION NUMBER: 31,8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: Herew CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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)GY: linear
                                       USA
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4370 La Jolla Village Drive, Suite 700
                                                                                                                   Genentech,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Herewith
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Pred. No. 1.3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 14;
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MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DoS/MS-DOS
SOPTWARE: patin (senentech)
CURRENT APPLICATION DATA:
APPLICATION UNMER: 91910315
CLASSIFICANION UNMER: 07/210,909
FILING DATE: 19910315
CLASSIFICANION DATA:
APPLICATION UNMER: 07/210,909
FILING DATE: JUNE 24,198
ATTORNEY/AGENT INFORMATION:
PRICE THANGE ANTE: JUNE 28,616
REFERENCE/DOCKET MUNBER: 513D1
TELECHONE: 415/952-9881
TELECHONE: 415/952-9881
TELECX: 910/371-7168
TELECX: 910/371-7
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Title:
Perfect score:
Sequence:
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No.
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Maximum DB
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Maximum Match
Listing first
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   protein search, using sw model
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g length: 17
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1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:*

2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*

3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*

4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*

5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*

6: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*

7: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:*

8: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:*
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96
1 FEHCNFNDVTTRLRENE 17
   348507 seqs, 71473746 residues
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Gapop 10.0 ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Copyright
                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2002, 09:23:56;
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100%
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US-09-989-919-123
US-10-006-869-1594
US-10-006-869-1597
US-09-579-174-21
US-09-754-831A-22
US-09-754-831A-22
US-09-701-080A-5
US-09-701-080A-5
US-09-701-080A-10
US-09-965-738-260
PCT-US02-08123-1760
US-10-038-612-114
US-08-816-4548-208
US-09-921-822-33
US-09-921-822-33
US-09-921-822-33
US-09-921-823-37
US-10-084-813-472
US-09-888-574-7
US-10-086-869-1592
PCT-US01-27702A-63
US-09-918-873-15
US-09-572-2708-58
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Sequence 123, App
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Sequence 21, Appl
Sequence 22, Appl
Sequence 387, Appl
Sequence 5, Appli
Sequence 10, Appl
Sequence 10, Appl
Sequence 116, Appl
Sequence 11760, App
Sequence 11760, App
Sequence 208, Appl
Sequence 33, Appl
Sequence 373, App
Sequence 422, Appl
Sequence 427, Appli
Sequence 427, Appli
Sequence 428, Appl
Sequence 4192, App
Sequence 429, App
Sequence 4192, App
Sequence 429, Appli
Sequence 50, Appli
Sequence 51, Appli
Sequence 51, Appl
                                                                                                                                                                                                                                                                                                    Description
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RESULT 2 US-10-006-869 ; Sequence 15 ; GENERAL INF ; APPLICANT: ; APPLICANT: ; APPLICANT: ; TITLE OF I ; TITLE OF I	Query Match Best Local Matches Qy 1 FEH Db 4 YKH	RESULT 1 US-09-989-919 Sequence 12 GENERAL INF APPLICANT: APPLICAN	
-1594 394, Applic ORMATION: Blaschuk, Symonds, Gour, Ba NVENTION:	tch al Similarity 3; Conserva FEHCNFNDVT 10 :: : ::: YKHCHMNNLS 13	3. App) 3. App) 3. App) 3. App) 3. App) 4. App) 4. App) 6. App) 6. App) 6. App) 7. App) 7. App) 8. App	22222222222222222222222222222222222222
ation US/ Orest W. James Ma irbara J. COMPOUNDS CADHERIN	32.3%; 30.0%; ative	+Q+++ b+ b	110 6 6 6 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
ation US/10006869 Orest W. James Matthew rbara J. COMPOUNDS AND METHODS FOR MODULATING CADHERIN-MEDIATED FUNCTIONS	Score 31; DB 6; Len Pred. No. 56; 6; Mismatches 1;	/09989919 tions and Methods Relating US/09/989,919 11-21 0/252,505 22 3.1	US-09-572-270B-62 US-09-572-270B-66 US-09-572-270B-70 US-09-572-240B-549 US-09-572-404B-3562 US-09-572-404B-3662 US-09-572-404B-3663 US-09-572-404B-3663 US-09-832-230A-67 US-10-083-768-67 US-10-083-768-67 US-10-095-549-28 US-09-711-161-14 US-09-711-084-813-421 US-10-084-813-421 US-10-084-813-421 US-10-084-813-417 US-10-084-813-418 US-09-350-641C-1523 US-10-084-813-418 US-09-350-641C-1523
ING NONCLASSICAL	gth 15; Indels 0; Gaps 0;	to Colon Specific Genes	Sequence 62, Appl Sequence 66, Appl Sequence 70, Appl Sequence 549, Appl Sequence 549, App Sequence 550, App Sequence 3662, App Sequence 3663, App Sequence 67, Appl Sequence 67, Appl Sequence 68, Appl Sequence 11, Appl Sequence 12, Appl Sequence 14, Appl Sequence 28, Appl Sequence 48, Appl Sequence 48, Appl Sequence 48, Appl Sequence 47, Appl Sequence 47, Appl Sequence 47, Appl Sequence 471, App Sequence 472, Appli Sequence 473, App

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US-09-579-174-21

Sequence 21, Application US/09579174

GENERAL INFORMATION:

APPLICANT: Guerinot, Mary Lou et al.

TITLE OF INVENTION: METAL-REGULATED TRANSPORTERS AND USES THEREFOR CURRENT APPLICATION NUMBER: US/09/579,174

CURRENT APPLICATION NUMBER: US/09/579,174

CURRENT FILING DATE: 2000-05-25

PRIOR APPLICATION NUMBER: 09/107,858

PRIOR APPLICATION NUMBER: 08/758,621

PRIOR APPLICATION NUMBER: 08/758,621

PRIOR APPLICATION NUMBER: 08/758,621

PRIOR PILING DATE: 1996-11-27

NUMBER OF SEQ ID NOS: 27

NUMBER OF SEQ ID NOS: 27
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SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 21
                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 71.4
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 3
US-10-006-869-1597
; Sequence 1597, A
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Best Local Similarity
""" ohes 5; Conserv.
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OTHER INFORMATION:
US-10-006-869-1594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 1597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1597, Application US/10006869
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Symonds, James Matthew
APPLICANT: Symonds, James Matthew
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
FILE REFERENCE: 100086.407C7
CURRENT APPLICATION NUMBER: US/10/006,869
RUMBER OF SEQ ID NOS: 4052
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Ver. SEQ ID NO 1594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Representative cyclic modulating agent based on OTHER INFORMATION: cadherin-8 cell adhesion recognition sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 100086.407C7
CURRENT APPLICATION NUMBER: US/10/006,869
CURRENT FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 4052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                      4 CNFNDVT 10
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                                                                                                                                                                                                                                                                                                                                       CQINDVT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                          31.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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2.9e+05;
2;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 9;
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                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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APPLICANIE OZNAYNAK, ENGIN
TITLE OF INVENTION: OSTEOGENIC DEVICES
FILE REFERENCE: STY-OOBCN
CURRENT APPLICATION UNMBER: U$/09/754,831A
CURRENT FILLING DATE: 2001-01-03
PRIOR APPLICATION NUMBER: U$ 08/375,901
PRIOR FILLING DATE: 1995-01-20
PRIOR FILLING DATE: 1993-11-01
PRIOR FILLING DATE: 1993-11-01
PRIOR APPLICATION NUMBER: U$ 07/995,345
PRIOR APPLICATION NUMBER: U$ 07/315,342
PRIOR FILING DATE: 1992-12-22
PRIOR FILING DATE: 1989-00-23
PRIOR FILING DATE: 1980-0-23
PRIOR FILING DATE: 1980-0-23
PRIOR FILING DATE: 1988-08-15
PRIOR APPLICATION NUMBER: U$ 07/312,630
PRIOR FILING DATE: 1988-08-15
PRIOR FILING DATE: 1980-0-23
                                                                                                                                                                                                                                                                                 В
                                                                                                                                                                                                       US-09-573-822C-387
                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Thes 4; Conserve
                                                             Sequence 387, Application US/09573822C
GENERAL INFORMATION:
APPLICANT: Proteom Ltd
TITLE OF INVENTION: Complementary peptide ligands generated from microbial genome
FILE REFERENCE: Microbe patent
CURRENT APPLICATION NUMBER: US/09/573,822C
CURRENT ETLING DATE: 2000-05-18
SEQ ID NO 387
LENGTH: 10
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: peptide fragment US-09-754-831A-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-754-831A-22
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Best Local Similarity
Watches 5; Conserve
                                          NUMBER OF SEQ ID NOS: 804
SOFTWARE: ProtPatent version 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn version 3.0 SEQ ID NO 22 LENGTH: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Arabidopsis thaliana US-09-579-174-21
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PRIOR FILLING DATE: 1988-04-08
NUMBER OF SEQ ID NOS: 72
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APPLICANT: Kuberasampath, T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
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TYPE: PRT
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45.5%;
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Pred. No. 86;
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; ORGANISM: mycoplasma genitalium; FEATURE:
; OTHER INFORMATION: Sequence located; OTHER INFORMATION: in this patent. US-09-573-822C-387
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Best Local Similarity
Watches 4; Conserv.
; OTHER INFORMATION: Description of Artificial Sequence:derived from US-09-701-080A-5
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; LOCATION: (1)..(13)
; OTHER INFORMATION: synthetic construct
PCT-US01-27692A-5
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Matches 5
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GENERAL INFORMATION:
APPLICANT: Board of Regents, The University of Texas System
TITLE OF INVENTION: Human and Mouse Targeting Peptides Identified by Phage Display
FILE REFERENCE: 005774.P003PCT
                                                                                                        NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                         Sequence 5, Application US/09701080A GENERAL INFORMATION:
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                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/701,080A CURRENT FILING DATE: 2001-02-27 PRIOR APPLICATION NUMBER: GB 9811303.8 PRIOR FILING DATE: 1998-05-26
                                                                                                                                                                                                                                                                       APPLICANT: O'CONNOR, MARK J.

APPLICANT: ZIMMERMAN, HOLLEER
TITLE OF INVENTION: POLYPEPTIDES FROM CREB BINDING PROTEIN AND RELATED PROTEIN P300
TITLE OF INVENTION: TRANSCRIPTIONAL REGULATION
FILE REFERENCE: 117-328
FILE REFERENCE: 117-328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: PCT/US01/27692A
CURRENT FILING DATE: 2001-09-07
NUMBER OF SEQ ID NOS: 251
                                                                                                                                                                                PRIOR APPLICATION NUMBER: GB 9900157.0
                                                                                                                                                               PRIOR FILING DATE: 1999-01-05
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                                   FEATURE:
                                                   ORGANISM: Artificial Sequence
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10 FEHC 13
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1.5e+02;
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GENERAL INFORMATION:

APPLICANT: O'Brien, Timothy

TITLE OF INVENTION: Repeat Sequences of the CA125 Gene and Their Use for Diagnosti

TITLE OF INVENTION: Therapeutic Interventions

FILE REFERENCE: 40715-258841

CUGRENT APPLICATION NUMBER: US/09/965,738

CURRENT FILING DATE: 2001-09-27

PRIOR APPLICATION NUMBER: US 60/284,175

PRIOR FILING DATE: 2001-04-17

NUMBER OF SEQ ID NOS: 306

COURTMANDER: DETORITE US 306
                                                                                                                                                                                    SOFTWARE: PatentIn version 3.0
SEQ ID NO 260
LENCTH: 12
TYPE: PRT
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Best Local Similarity
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Best Local
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TITLE OF INVENTION: POLYPEPTIDES FROM CREB BINDING PROTEIN AND RELATED PROTEIN P30
TITLE OF INVENTION: TRANSCRIPTIONAL REGULATION
FILE REFERENCE: 117-328
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ORGANISM: Artificial Sequence
                                                                                                                                                                   ORGANISM: Homo sapiens
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1 FTHRNFVPITS 11
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Pred. No. 1.5e
2; Mismatches
                                                                   Score 27; DB Pred. No. 2.1e 2; Mismatches
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Pred. No. 1
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1.5e+02;
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TITLE OF INVENTION: Short Peptides which Selectively
TITLE OF INVENTION: Modulate the Activity of Protein Kinases
FILE REFERENCE: 1242.1029-000 (CMCC-679)
CURRENT APPLICATION NUMBER: US/10/038,612
PRIOR APPLICATION NUMBER: US/10/038,612
PRIOR APPLICATION NUMBER: US/09/161,094
PRIOR FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 172
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 16
TYPE: PRT
                                                                                        RESULT 13
US-10-038-612-114
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Best Local Similarity
Thehes 5; Conserva
Sequence 11, Application US/10038612
GENERAL INFORMATION:
APPLICANT: Ben-Sasson, Shmuel A.
TITLE OF INVENTION: Short Peptides Which Selectively
TITLE OF INVENTION: Modulate the Activity of Protein Kinases
                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: CK IIa US-10-038-612-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/331,287
PRIOR FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/306,171
PRIOR ETLING DATE: 2001-07-19
PRIOR PRIOR APPLICATION NUMBER: US 60/277,340
PRIOR ETLING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 2048
SEQ ID NO 1760
SEQ ID NO 1760
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GENERAL INFORMATION:
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; Sequence 1760, Apr
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APPLICANT: Human Genome Sciences, Inc.
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71.4%;
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Pred. No. 2.
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2.9e+02;
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US-08-816-454B-208
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TYPE: PRT
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Sequence 208, Applicat GENERAL INFORMATION: APPLICANT: SLIN
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PRIOR FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 172
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: MYRISTATE
LOCATION: (1)...(0)
NAME/KEY: AMIDATION
LOCATION: (0)...(17)
OTHER IMPORMATION: CK IIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 1242.1029-000 (CMCC-679) CURRENT APPLICATION NUMBER: US/10/038.612 CURRENT FILING DATE: 2002-01-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial
                 NAME: COOPER, IVER P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: SL:
TELECOMMUNICATION: INFORMATION:
TELEPHONE: (202) 628-5197
                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/027,627
FILING DATE: 04-0CT-1996
APPLICATION NUMBER: US 60/013,972
FILING DATE: 19-MAR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patenth Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
les 5; Conser
                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENGELIARD, VICTOR H.

KITTLESEN, David
SKIPPER, Jonathan
SKIPPER, Jonathan
HENDRIKSON, Ronald C.

TITLE OF INVENTION: PEPTIDES RECOGNIZED BY MELANOMA-SPECIFIC
Al-, A2, A3-RESTRICTED CYTOTOXIC LYMPHOCYTES AND USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/816,454B FILING DATE: 12-Mar-1997
                                                                                                                                                                                                                                CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: BROWDY AND NIEMARK, P.L.L.C. STREET: 624 Ninth Street N.W., Ste. 300
                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/08816454B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLINGLUFF, Craig L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COX, Andrea L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HUNT, Donald F. SHABANOWITZ, Jeffrey
(202) 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 27; DB 7; Len
Pred. No. 3.1e+02;
^v:cmatches 3;
                                                         SLINGLUFF=2/3
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INFORMATION FOR SEQ ID NO: 208: SEQUENCE CHARACTERISTICS:

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RESULT 15
US-09-921-822-33
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US-09-921-822-33
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APPLICANT: Schatz,
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                       TELEFAX: 415-326-2422 INFORMATION FOR SEQ ID NO: 33:
                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/290,641
FILING DATE: 15-AUG-1994
APPLICATION NUMBER: US 07/963,321
FILING DATE: 15-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 16528J-0012
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
FETTERENCE - 157-526-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cull, Millard G.

Miller, Jeff F.

Stemmer, Willem P.C.

Stemser, Christian M.

TITLE OF INVENTION: Peptide Library and Screening Method
NUMBER OF SEQUENCES: 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/504,787
FILING DATE: <Unknown>
                  SEQUENCE DESCRIPTION: SEQ ID NO: 33:
                                                  STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: peptide IMMEDIATE SOURCE:
                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 12 amino acids
TYPE: amino acid
                                                                                                                                LENGTH: 12 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/921,822 FILING DATE: 02-Aug-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: William M. Smith STREET: One Market Plaza, Steuart Tower, Suite 2000
                                      CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
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66.78;
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Pred. No.
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CURRENT APPLICATION NUMBER: US/10/084,813
CURRENT FILING DATE: 2002-02-27
PRIOR APPLICATION NUMBER: PCT/US00/23505
PRIOR FILING DATE: 2000-08-25
PRIOR APPLICATION NUMBER: US 60/151,270
PRIOR FILING DATE: 1999-08-27
NUMBER OF SEQ ID NOS: 1242
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 422
LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-084-813-422; Sequence 422, Applic: GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: binding peptide 05\text{-}09\text{-}954\text{-}385\text{-}373
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                                                                          US-10-084-813-422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 433
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 373
TENERM.
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Best Local Similarity
Matches 5; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Baldwin, Toby L.
APPLICANT: Van Gastel, Franciscus J.C.
APPLICANT: Janssen, Giselle G.
APPLICANT: Murray, Christopher J.
APPLICANT: Wang, Huaming
APPLICANT: Winetzky, Deborah S.
TITLE OF INVENTION: Binding Phenol Oxidizing Enzyme-peptide
TITLE OF INVENTION: Complexes
                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE FILE REFERENCE: 215875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: GC690
CURRENT APPLICATION NUMBER: US/09/954,385
CURRENT FILING DATE: 2001-09-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Aehle, Wolfgang
APPLICANT: Baldwin, Toby L.
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: SAXINGER, CARL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                           ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                TYPE: PRT
                                                                                          OTHER INFORMATION: Description of Artificial Sequence: binding peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 VTQRVRSNK 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 NESNVSTK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 NFNDVTTR 12
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55.6%;
27.1%;
50.0%;
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Pred. No.
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Pred. No. 3.1e+02;
Score 26;
Pred. No.
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Query Match Best Local Similarity

DB 7; 3.1e+02;

Length 12;

В δÃ

G

Matches

Sequence 7

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Query Match
Best Local Similarity
""" 4; Conserve
                                                                                                                                                                                                                                        ; OTHER INFORMATION: Description of Artificial Sequence: binding peptide US-10-084-813-419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-084-813-419

Sequence 419, Application US/10084813

GENERAL INFORMATION:
APPLICANT: SAXINGER, CARL
TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
FILE REFERENCE: 215875
                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/084,813
CURRENT FILING DATE: 2002-02-27
PRIOR APPLICATION NUMBER: PCT/US00/23505
PRIOR FILING DATE: 2000-08-25
PRIOR APPLICATION NUMBER: US 60/151,270
PRIOR FILING DATE: 1999-08-27
NUMBER OF SEO ID NOS: 1242
SOFTWARE: PATENTIN VETSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT; ORGANISM: Homo sapiens US-09-828-574-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-828-574-7
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Best Local Similarity 35.7
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn version 3.1 SEQ ID NO 7
                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/828,574
CURRENT FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: US 60/224,104
PRIOR FILING DATE: 2000-08-09
NUMBER OF SEQ ID NOS: 13
CODDMIANDE: Datasets 3 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: ALBANI, Salvatore
APPLICANT: PRAKKEN, Berent J.
TITLE OF INVENTION: STRESS PROTEINS AND PEPTIDES AND METHODS OF USE THEREOF
FILE REFERENCE: UCSD1310-1
                                                                                 8 ENANFNKI 15
                                                                                                                2 EHCNFNDV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 CEFQDAYVLLSEKK 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              e 7, Application US/09828574 INFORMATION:
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50.0%;
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35.7%;
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Pred. No.
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Pred. No.
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, 3.9e+02;
8;
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3.9e+02;
2;
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                                                                                                                                                                        Length 15
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Best Local Similarity
"arches 4; Conserv:
                                                                                                                                                             RESULT
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LOCATION: (1). (8)
OTHER INFORMATION: synthetic construct
PCT-US01-27702A-63
     Sequence 15, Application US/09918873
GENERAL IMFORMATION:
APPLICANT: Goldsmith, Elizabeth J.
APPLICANT: Radha, Akella
APPLICANT: Gaynor, Richard B.
TITLE OF INVENTION: CHIMERIZING PROTEIN KINASES FOR DRUG
TITLE OF INVENTION: DISCOVERY
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CURRENT FILING DATE: 2001-09-07.
NUMBER OF SEQ ID NOS: 273
SOFTWARE: Patentin version 3.1
SEQ ID NO 63
LENGTH: 8
TURNS NEWS
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; Sequence 1592, Application US/10006869
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 63, Application PC/TUS0127702A
GENERAL INFORMATION:
APPLICANT: Board of Regents, The University of Texas System
TITLE OF INVENTION: Methods and Compositions for In Vitro Targeting
FILE REFERENCE: 005774, P005PCT
CHERENUM ADDITION MINUSED: COM JOSEPH
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Best Local :
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SEQ ID NO 1592
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Blaschuk, Orest W.
APPLICANT: Symonds, James Matthew
APPLICANT: Symonds, James Matthew
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
FILE REFERENCE: 100086.407C7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/006,869
CURRENT FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 4052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Representative cyclic modulating agent based on OTHER INFORMATION: cadherin-8 cell adhesion recognition sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence FEATURE:
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57.1%;
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66.7%;
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Pred. No. 2.9e+05;
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2.9e+05;
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LENGTH: 15

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SEQ ID NO 419

LENGTH: 15 TYPE: PRT

Gaps

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US-09-572-270B-54
; Sequence 54, Application US/09572270B
; GENERAL INFORMATION:
APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from plant genomes
; FILE REFERENCE: Plant patent
; CURRENT APPLICATION NUMBER: US/09/572,270B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 1144
; NUMBER OF SEQ ID NOS: 1144
; OTHER INFORMATION: Sequence located in CAD1. at 36-45 and may interact with Sequence; OTHER INFORMATION: this patent. US-09-572-270B-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
; DATABASE ACCESSION NUMBER: 18158777
; DATABASE ENTRY DATE: 2001-01-29
US-09-918-873-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Sequence located in CAD1. at 36-45 and may interact with Sequence; OTHER INFORMATION: this patent. US-09-572-270B-50
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GENERAL INFORMATION:
APPLICANT: Proteom Ltd
TITLE OF INVENTION: Complementary peptide ligands from plant genomes
FILE REFERENCE: Plant patent
CURRENT APPLICATION NUMBER: US/09/572,270B
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 1144
SOFTWARE: ProtPatent version 1.0
SEQ ID NO 50
LENGTH: 10
                                                                                                      SOFTWARE: ProtPatent version 1.0
SEQ ID NO 54
LENGTH: 10
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15
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Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
Matches 3; Conserv
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CURRENT FILING DATE: 2002-07-31
                                                                     TYPE: PRT
ORGANISM: Arabidopsis Thaliana
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Pred. No. 2.9e+05;
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3.7e+02;
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Search completed: April
Job time: 183 sec
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                                                                                                                                                                                                                                                                                         SOFTWARE: ProtPatent version 1.0 SEQ ID NO 58 LENCTH: 10 TYPE: PRT
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APPLICANT: Proteom Ltd
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Best Local Similarity
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Complementary peptide ligands from plant genomes FILE REFERENCE: Plant patent CURRENT APPLICATION NUMBER: US/09/572,270B
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 1144
                                                                                                                                                                                                                                                            ORGANISM: Arabidopsis Thaliana FEATURE:
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                                                                                                     7 NDVTTRL 13
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57.1%;
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Pred. No. 3.7e+02;
2; Mismatches 1
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Pred. No. 3.7e+02;
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Perfect score:
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length: 17
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/Backfiles1.pep:*
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     2002, 09:22:51; Search time 12.51 Seconds (without alignments) 30.580 Million cell updates/sec
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 US-08-460-309-23
US-08-152-077-23
5444158-4
US-08-556-597-13
US-08-556-597-13
US-08-685-357B-12
US-08-952-568-20
5194585-1
5194585-3
US-08-218-025A-105
US-09-224-785-22
US-09-224-785-25
US-07-778-233B-25
US-07-78-233B-33
US-07-963-321-3
US-07-963-321-3
US-08-413-708B-5
US-08-413-708B-5
US-09-164-133
US-08-413-708B-5
US-09-164-186-5
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US-09-231-159-16

US-08-611-307-16

US-08-758-621-21

US-09-107-858-21

5496552-8
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Sequence 21, Appl
Sequence 23, Appl
Sequence 23, Appl
Sequence 23, Appl
Sequence 6, Appl 1,
Sequence 133, Appl
Sequence 12, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 20, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 33, Appl
Sequence 34, Appl
Sequence 25, Appli
Sequence 26, Appli
Sequence 27, Appli
Sequence 28, Appli
Sequence 29, Appli
Sequence 29, Appli
Sequence 21, Appli
Sequence 22, Appli
Sequence 23, Appli
Sequence 24, Appli
Sequence 25, Appli
Sequence 26, Appli
Sequence 27, Appli
Sequence 27, Appli
Sequence 28, Appli
Sequence 29, Appli
Sequence 21, Appli
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Sequence 16, Appl
Sequence 16, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
Patent No. 5496552
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25.0	25.0	5	6	σ.	26.0	σ.	6.	6.	26.0	٥.	6.	6.	26.0	6.	6.	26.0	6.	6.	6.	6.	26.6	6.
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US-09-518-046-74	PCT-US91-02166-14	US-08-672-610A-53	US-09-082-279B-848	PCT-US95-05657-1	PCT-US95-04018-19	PCT-US95-04018-18	PCT-US95-04018-17	US-08-310-341B-1	US-08-221-583-19	US-08-221-583-18	US-08-221-583-17	US-09-196-390-8	US-08-836-567-17	US-09-224-785-29	US-09-516-704-67	US-09-244-298A-67	US-08-973-225-67	US-08-764-640-67	US-09-502-600-69	US-08-375-911A-5	US-08-590-563-22	US-08-468-812-14
Sequence 74, Appl	Sequence 14, Appl	Sequence 53, Appl	Sequence 848, App	Sequence 1, Appli	Sequence 19, Appl	Sequence 18, Appl	Sequence 17, Appl	Sequence 1, Appli	•	Sequence 18, Appl	Sequence 17, Appl	Sequence 8, Appli	Sequence 17, Appl	•	•	Sequence 67, Appl	•	Sequence 67, Appl	Sequence 69, Appl	Sequence 5, Appli	Sequence 22, Appl	Sequence 14, Appl

ALIGNMENTS

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RESULT 1
US-08-232-513A-11
                                                                                                        APPLICATION NUMBER: US/08/232,513A
FILING DATE: 21-APR-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 08/100,247
FILING DATE: 30-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: P-UD 1643
REFERENCE/DOCKET NUMBER: P-UD 1643
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-901
TELEPAX: (619) 535-8949
INFORMATION FOR SEO ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acids
TYPE: amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: O'Brien, Joh
TITLE OF INVENTION: Pro
TITLE OF INVENTION: as
                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 4370 La Jo
CITY: San Diego
STATE: California
NAME/KEY: Peptide LOCATION: 1..17 OTHER INFORMATION:
                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Campbell & Flores LLP
4370 La Jolla Village Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                  linear
                                                                            peptide
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    /label= hEPO
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US-08-232-513A-11

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US-08-611-307-16
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                                                  Sequence 16, Application US/08611307 Patent No. 6271196
GENERAL INFORMATION:
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US-09-231-159-16
                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
CLASSIFICATION:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US-96/231,159
FILIME DATE: 05-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Campbell Cathryn A.
REGISTRATION NUMBER: 31,815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTY...
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
TOMPUTER: TBM PC COMPATIBLE
TO ASSE #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No. 6268347
GENERAL INFORMATION:
APPLICANT: O'Brien, John S.
                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (619) 535-90
TELEPAX: (619) 535-8949
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 16, Application US/09231159 Patent No. 6268347
         APPLICANT: O'Brien,
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local ;
 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: P-UD 1928
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRINT APPLICATION DATA:
APPLICATION UMBER: US/09/231,159
FILING DATE:
                                                                                                                                                                                                                   Local Similarity
les 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 4370 La Jo
CITY: San Diego
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 2. CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                              N
                                                                                                                                                                                     2 EHCNFNDVTT 11
                                                                                                                                                                                                                                                                                                                               LENGTH:
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                                                                                                                                                         EHCSLNENIT 11
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                                                                                                                                                                                                                                                                                                  amino acid
)GY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 5; Conserv
                                         O'Brien,
                                                                                                                                                                                                                                                                                                                           17 amino acids
                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Campbell and Flores
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
Using Prosaposin-Derived
                   John S.
Methods of Alleviating
                                                                                                                                                                                                                           33.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Using Prosaposin-Derived Peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Methods of Alleviating Neuropathic Pain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33.3%;
                                                                                                                                                                                                                           Score 32; DB
Pred. No. 28;
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Pred. No.
                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                  DB 4; Length 17;
                  Neuropathic Pain
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US-08-758-621-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: US-08-611-307-16
NAME: Silveri, Jean M.
REGISTRATION NUMBER: 39,030
REFERENCE/DOCKET NUMBER: DCI-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 21, Application US/08758621 Patent No. 5846821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/758,621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
                                                                                                FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/018,578

FILING DATE: 29-MAY-1996

ATTORNEY/AGENT INFORMATION:

NAME: Silveri, Jean M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM FLOWPY CLISK
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-D
SOFTWARE: Patentin Release #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/611
ETILING DATE: 05-MAR-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 9-UD
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Guerinot, TITLE OF INVENTION: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTILE OF INVENTION: Metal-Regulated Transporters and Uses Therefor NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 60 St
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
les 5; Conserv
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CITY: San Diego
STATE: Californi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EHCNFNDVTT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                60 State Street
                                                                                                                                                                                                                                                                                                                                                                 USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Release #1.0, Version #1.25
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                                                         DCI-099CP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 32;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ed. No. 28;
Mismatches
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INFORMATION FOR SEQ ID NO:

21:

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Query Match
Best Local Similarity
5; Conserve
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5496552-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Arabidopsis thaliana US-09-107-858-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-107-858-21
                                                   5496552-8
                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                             Patent No. 5496552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Guerinot, Mary Lou et al.
APPLICANT: Guerinot, METAL-REGULATED TRANSPORTERS AND USES THEREFOR
TITLE OF INVENTION: METAL-REGULATED TRANSPORTERS AND USES THEREFOR
FILE REFERENCE: DCI-099CPDV
CURRENT FILING DATE: 1998-06-30
CURRENT FILING DATE: 1998-06-30
EARLIER APPLICATION NUMBER: 08/758,621
EARLIER APPLICATION NUMBER: 08/758,621
EARLIER FILING DATE: 1996-11-27
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 21
FENCTU- 16
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Best Local Similarity
Matches 5; Conserv
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Patent No. 6162900
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1:
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS LENGTH: 16 amino acids
                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/(
FILING DATE: 29-JUN-1994
                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                           APPLICANT: KUBERASAMPATH, THAN TITLE OF INVENTION: OSTEOGENIC
                                                                                                                            APPLICATION NUMBER: 103,604
FILING DATE: 06 AUG-1993
APPLICATION NUMBER: 827,052
FILING DATE: 28 JAN-1992
APPLICATION NUMBER: 579,865
FILING DATE: 07-SEP-1990
                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                  LENGTH: 11
                                                                                                                  APPLICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 NDVTTRLRENE 17
                                                                                                                                                                                                                                                                                                                                                                                                                               3 NDVTLPIKEDD 13
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                                                                                            NUMBER: 179,406
08-APR-1988
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45.5%;
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30.2%;
                                                                                                                                                                                                                                                           US/08/268,252
                                                                                                                                                                                                                                                                                                            THANGAVEL; RUEGER, DAVID C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 30;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 30; DB Pred. No. 57;
Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
29;
DB
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6;
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Length 11;
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RESULT 7
US-08-460-309-23
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                                                      Db
                                                                                                            Query Match
Best Local Similarity
Thes 5; Conserva
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RESULT
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,309
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/125,077
FILING DATE: 22-SEP-1993
APPLICATION NUMBER: US PCT/US 94/10730
FILING DATE: 21-SEP-1994
PRIOR APPLICATION NUMBER: US PCT/US 94/10730
FILING DATE: 21-SEP-1994
PRIOR APPLICATION NUMBER: US 07/472,319
FILING DATE: 30-JAN-1990
FILING DATE: US 07/472,319
FILING DATE: US 07/472,319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 23, Applipatent No. 5837496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 50.0 Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                          TELEFAX: (619) 535-8949 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 07/919,951 FILING DATE: 27-JUL-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPUTER: IBM PC COMPONIALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: P-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 43. CITY: San Diego
CITY: San Diego
CTATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin TITLE OF INVENTION: Fragments and Uses Thereof NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Engvall, Eve
APPLICANT: Leivo, Ilmo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                           TYPE: a
                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Campbell, Cathryn A. REGISTRATION NUMBER: 31,81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 FEHCNFND 8
                                                    1 CSIVDIDTNQEEN 13
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                                                                                         4 CNFNDVTTRLREN 16
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                                                                                                                                                                                                                                                        amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Campbell and Flores
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                           14 amino acids
                                                                                                                             Conservative
                                                                                                                                               30.2%;
38.5%;
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                                                                                                                                             Score 29; DB 2; Pred. No. 72;
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2; Mismatches
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                                                                                                                                                                Length 14;
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; Sequence 23, Application US/08125077
; Patent No. 5872231

US-08-125-077-23

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RESULT 9
5444158-4
;Patent NO. 5444158
; Patent NO. 5444158
; PATENT OF INVENTION: MEROSIN, NUCLEIC ACIDS ENCODING,
;FRAGMENTS AND USES THEREOF
;NUMBER OF SEQUENCES: 4
;CURRENT APPLICATION DATA:
;CURRENT APPLICATION DATA:
                            SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-125-077-23
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION DATA:
APPLICATION UNMBER: US/08/125,077
FILING DATE: 22-SEP-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US PCT/US 94/10730
FILING DATE: 21-SEP-1994
PRIOR APPLICATION NUMBER: US 07/472,319
FILING DATE: 30-JAN-1990
PRIOR APPLICATION DATA: US 07/472,319
FILING DATE: 30-JAN-1990
PRIOR APPLICATION NUMBER: US 07/919,951
FILING DATE: 27-JUL-1992
ATTORNEY/ACENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: P-LA 9721
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-9001
                                                                                                     APPLICATION NUMBER: US/C
FILING DATE: 08-JUL-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No. 5872231 5840863
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LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION
                                                    APPLICATION NUMBER: 587,689
FILING DATE: 24-SEP-1990
APPLICATION NUMBER: 472,319
                          FILING DATE:
NO:4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin TITLE OF INVENTION: Fragments and Uses Thereof NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
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les 5; Conserv
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APPLICANT: Leivo, Ilmo
                                                                                                                                                                                                                                                                                                                                                                        4 CNFNDVTTRLREN 16
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CITY: S
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                                         30-JAN-1990
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70 La Jolla Village Drive, Suite 700
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                                                                                                                                          US/08/87,642
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Pred. No.
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       Query Match
Best Local Similarity
Matches
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В δÃ

Conservative

29.2%;

Score 28; DB 1; Pred. No. 1.1e+02; Mismatches

Length 15; Indels

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Gaps

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US-08-522-326-6
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US-08-522-326-6
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Best Local Similarity
"~+~hes 5; Conserva
                                                                                                                                                                                                                                         TELEFAX: (202) 371-254
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/08522326 Patent No. 5753615
                                                OTHER INFORMATION: /product= "OTHER"
OTHER INFORMATION: /note= "pyro-glut
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                            MOLECULE TYPE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 20005-55.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9:
FILING DATE: 12-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: LUDWIG, STEVEN R.
                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING COLOR OF THE PROPERTY APPLICATION DATA:
CURRENT APPLICATION DATA:
US/08/522,326
       DOCUMENT NUMBER: WO 94/20530 A2 FILING DATE: 14-MAR-1994 PUBLICATION DATE: 15-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: THORPE
APPLICANT: DUVE,
APPLICANT: JOHNSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                    LOCATION:
                                                                                                             NAME/KEY: Modified-site
                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                         ORGANISM: Manduca sexta
                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                           TELEPHONE:
                                                                                                                                                                                                                                                                                                                                       NAME: LUDWIG, STEVEN R. REGISTRATION NUMBER: 36
                                                                                                                                                                                                                                   LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/01
FILING DATE: 12-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: US
ZIP: 20005-3934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 1100 NEW CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
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                                                                                                                                                                                       linear
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VENTION: NEUROPEPTIDES AND THEIR USE AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       THORPE, Alan
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38.5%;
                                                              _note= "pyro-glutamic acid"
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Pred. No. 72;
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; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-556-597-133
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Best Local Similarity
Thes 6; Conserve
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US-08-556-597-133
                                                                                                                                                                                    US-08-685-357B-12
                                                                                                                                                                                                       RESULT 12
                                                                                                           Patent No. 5854216
GENERAL INFORMATION:
APPLICANT: GAUDRE
                                                                                                                                                 Sequence 12, Application US/08685357B Patent No. 5854216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 133, Application US/08556597 Patent No. 5877155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (716) 263-1600 INFORMATION FOR SEQ ID NO: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Timlan, Susan J.
REGISTAN NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Miller, Jonathan L.
APPLICANT: Lyle, Vicki A.
TITLE OF INVENTION: HUMOTOPES AND ANTI-MIMOTOPES OF
TITLE OF INVENTION: HUMAN PLATELET GLYCOPROTEIN ID/IX
NUMBER OF SEQUENCES: 173
                                                                        APPLICANT: GAUDREAU, Pierrette
TITLE OF INVENTION: MARKER FOR GROWTH HORMONE-RELEASING
TITLE OF INVENTION: FACTOR RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/406,330 FILING DATE: 17-MAR-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                    NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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CITY: Rochester
 STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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                   ADDRESSEE:
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E: Kevin M. Farrell, P.C. 12 Riverwood Drive - P.O. Box 999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 amino acids
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Pred. No. 8
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; MOLECULE TYPE:
; HYPOTHETICAL: N
US-08-685-357B-12
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Best Local Similarity
Watches 5; Conserve
US-08-952-568-20
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                                                                                                                                                                                                                                                                                                                                                                                               Sequence 20, Application US/08952568 Patent No. 6037321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 514
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/312,
FILING DATE: 23-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: FARRELL, Kevin M.
REGISTRATION NUMBER: 35,505
                                                                                                                                FILING DATE: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (207) 363-055
TELEFAX: (207) 363-0528
INFORMATION FOR SEQ ID NO:
                                                                                                                                                               FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 35,505
TELECOMMUNICATION INFORMATION:
TELEPHONE: (207) 363-0558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/685,357B
                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
               MOLECULE TYPE:
FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Vasoactive Intestinal Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: M
                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Palan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
                                                 TOPOLOGY:
                                                             STRANDEDNESS:
                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
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                                                                              amino acid
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internal
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                                                                                                                                                                  PCT/CA96/00280
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                                                                                                                                                                                                                                                 Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
1.3e+02;
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Query Match Best Local Similarity

28.1%; 60.0%;

Score 27; Pred. No.

DB 3; 1.3e+02;

Length 12;

RESULT 14 5194585-1

Patent No. 5194585;

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Matches

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Conservative

1;

Mismatches

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Query Match
Best Local Similarity 60.00
""" hohes 6; Conservative
                                     GENERAL INFORMATION:
APPLICANT: Weiner, David B.
APPLICANT: Ugen, Kenneth E.
APPLICANT: Williams, William v.
TITLE OF INVENTION: Methods and Compositions for Diagnosing
TITLE OF INVENTION: and Treating Certain HIV Infected Patients
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                   Sequence 105, Application US/08218025A
Patent No. 5556744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MASSEY, RICHARD J.

TITLE OF INVENTION: INHIBITORS OF CATALYTIC ANTIBODIES
NUMBER OF SEQUENCES: 13
CURRENT APPLICATION DATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: INHIBITORS OF CATALYTIC ANTIBODIES NUMBER OF SEQUENCES: 13
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/486,594
PILING DATE: 28-FEB-1990
PATOR APPLICATION DATA:
APPLICATION NUMBER: 343,081
FILING DATE: 25-ADR-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: PAUL, SUDHIR; POWELL, MICHAEL J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/07/486,594
FILING DATE: 28-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 343,081
FILING DATE: 25-APR-1989
ID NO:1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: PAUL, SUDHIR; POWELL, MICHAEL J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28.1%;
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60.0%;
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Pred. No. 1.8e+02;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
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Pred. No. 1.8e+02;
1; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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Query Match
Best Local Similarity
""" ohes 3; Conserve
                                                                                                                                                   ; OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: binding loop peptide US-09-224-785-22
                                                                                                                                                                                                                                                                                                          SOFTWARE: P
SEQ ID NO 22
LENGTH: 11
TYPE: PRT
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; MOLECULE TYPE: peptide
US-08-218-025A-105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECHONE: (215) 540-5818
TELEFAX: (215) 540-5818
TELEFAX: (215) 10 NO: 10
SEQUENCE CHARACTERISTICS:
"FMGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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Patent No. 6197526
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Yu, Jinan
APPLICANT: Kelley, Brian D
APPLICANT: Leetz, Jeffrey S
APPLICANT: Deetz, Jeffrey S
APPLICANT: Booth, James E
TITLE OF INVENTION: Binding Molecules for Human Factor VIII and Factor
TITLE OF INVENTION: VIII-like Proteins
FILE REFERENCE: Dyax-008 US sequence listing
CURRENT APPLICATION NUMBER: US/09/224,785A
NUMBER OF SEO ID NOS: 46
SOFTWARER SECOND SEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION UNMBER: US/08/218,025A FILING DATE: 24-MAR-1994 CLASSIFICATION: 424 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/891,451 FILING DATE: 29-MAY-1992 ATTORNEY/AGENT INFORMATION: NAME: Bak, Mary E. REGISTRATION NUMBER: WST33A TELECOMMUNICATION INFORMATION: TELEPHONE: (215) 540-9206
                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
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1 CSFN-ISTSIR 10
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STATE: Pennsylvania
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                               PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Potter, M. Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19477
                       Conservative
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                                                 27.1%;
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45.5%;
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           Score 26; DB 4; Len
Pred. No. 1.7e+02;
Pred. No. 1.7e+02;
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Pred. No. 2e+02;
4; Mismatches
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              Indels
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RESULT 16 US-08-218-025A-105

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SEQ ID NO:3: LENGTH: 16

RESULT 1 5194585-3

Patent No. 5194585

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5194585-1

LENGTH: 16

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RESULT 19
US-07-778-233B-33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-224-785-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 33, Application US/07778233B Patent No. 5270170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Potter, M. Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 25, Application US/09224785A Patent No. 6197526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Binding Molecules for Human Factor VIII and Factor TITLE OF INVENTION: VIII-like Proteins
FILE REFERNCE: Dyax-000 US sequence listing
CURRENT APPLICATION NUMBER: US/09/224,785A
CURRENT FILING DATE: 1999-01-04
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/778,233B
FILING DATE: 19911016
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                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Schatz, Peter J.
APPLICANT: Cull, Millard G.
APPLICANT: Miller, Jeff F.
TITLE OF INVENTION: Peptide Library and Screening Method
NUMBER OF SEQUENCES: 78
              CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11:
                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                    COUNTRY: UZIP: 94105
                                                                                                                                                                                                                                                                                                                                              CITY: San Francisco
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                                                                                                                                                                                                                                                                                                                         California
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Deetz, Jeffrey S
Booth, James E
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60.0%;
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Query Match

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; CLONE: 7 4 1.1
US-07-778-233B-33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 5338665
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity Matches 5; Conserv
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                                                                                                     TELEFAX: 415-326-2422 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                APPLICATION NUMBER: US 0:
FILING DATE: 16-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,;
                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
MOLECULE TYPE: FIMMEDIATE SOURCE: 7 4 1.1
                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
                                                                                                                                                  REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Stemmer, Willem P.C.
TITLE OF INVENTION: Peptide Library and Screening Method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                          TOPOLOGY:
                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: UPFILING DATE: 19921015
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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                                                                                    LENGTH:
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                                                                       AMINO ACID
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                                                                                      12 amino acids
                                                                                                                                     415-326-2422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 1.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Miller, Jeff F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schatz, Peter J. Cull, Millard G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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                                          linear
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                                                                                                                                                                                                                                                                                                                                                                                                     Floppy disk
                          peptide
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                                                                                                                                                                                                                                                                 US 07/778,223
                                                                                                                                                                                                 30,223
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Local Similarity 55.6 hes 5; Conservative

55.6%;

US-08-290-641-33

GENERAL INFORMATION:

COUNTRY:

USA

California

94105

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1 VTORVRSNK 9

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VITRLRENE 17

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RESULT 22
US-08-548-540-33
; Sequence 33, Application US/08548540
; Patent No. 5733731
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 07/963,321
FILING DATE: 15-OCT-1992
APPLICATION NUMBER: US 07/778,223
APPLICATION NUMBER: US 07/778,223
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11509-50-
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 176-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 33, Application US/08290641 Patent No. 5498530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM_PC COMPATIBLE
OPERATING SYSTEM: PC-DOS_MS-DOS
SOFTWARE: PATENTIAN PLOCATION DATA:
APPLICATION NUMBER: US/08/290,641
FILING DATE: 15-AUG-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 91

CORRESPONDENCE ADDRESS:
ADDRESSE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Schatz, Peter J.
APPLICANT: Cull, Millard G.
APPLICANT: Miller, Jeff F.
APPLICANT: Stemmer, Willem P.C.
TITLE OF INVENTION: Peptide Library and Screening Method
                                                                                                                                                                                                                    Score 26; DB 1;
Pred. No. 1.9e+02;
2; Mismatches 2
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2; Mismatches 2;
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                                                                                                                                                                                                                                                    Length 12;
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                                                                                                                                                                                                                Sequence 33, Application PC/TUS9609809 GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/290,641
FILING DATE: 15-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,321
FILING DATE: 15-CCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 30,223
TELECHMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
                                                     APPLICANT: Schatz, Peter J.
APPLICANT: Cull, Millard G.
APPLICANT: Miller, Jeff F.
APPLICANT: Stemmer, Willem P.C.
APPLICANT: Gates, Christian M.
TITLE OF INVENTION: Peptide Library and Screening Method NUMBER OF SEQUENCES: 162
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMMEDIATE SOURCE:
CLONE: 7 4 1.1
 CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/548,540
FILTING NAME: 05/08/548,540
                          ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Miller, Willem P.C.
APPLICANT: Stemmer, Willem P.C.
APPLICANT: Gates, Christian M.
TYPE OF INVENTION: Peptide Library and Screening Method
                                                                                                                                                                                                                                                                                                                            1 VTORVRSNK 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                             9 VTTRLRENE 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENGTH:
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California
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One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schatz, Peter J.
Cull, Millard G.
Miller, Jeff F.
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Pred. No. 1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                         Length 12;
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VTTRLRENE 17

1 VTQRVRSNK 9

Query Match
Best Local Similarity
Thehes 5; Conserve

Conservative

27.1%; 55.6%;

US-08-290-641-33

IMMEDIATE SOURCE: CLONE: 7 4 1.1

MOLECULE TYPE:

TOPOLOGY:

linear

TELEFAX: 415-326-2422 NFORMATION FOR SEQ ID NO:

SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single

CURRENT APPLICATION DATA:

COMPUTER READABLE FORM: MEDIUM TYPE: Floppy

COUNTRY:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

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Best Local Similarity
~~+~hes 5; Conserv
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US-08-413-708B-5
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                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/08413708B Patent No. 5972883
                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: GOZES, Illana
APPLICANT: FRIDKIN, Matityahu
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS COMPRISING
TITLE OF INVENTION: VIP, OR ANALOGUES DERIVATIVES AND FRAGMENTS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/548,540
FILING DATE: 26-OCT-1995
APPLICATION NUMBER: US 08/290,641
FILING DATE: 15-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 15-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,321
FILING DATE: 15-OCT-1992
                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMMEDIATE SOURCE
CLONE: 7 4 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                           STREET: 419 Sever CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION:
APPLICATION NUMBER: US/01 FILING DATE: 30-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                 COUNTRY: UZIP: 20004
                                                                                                                                                                                                                                          ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VTQRVRSNK 9
                                                                                                                                                                                                                E: BROWDY AND NEIMARK
419 Seventh Street, N.W., Suite 300
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                                                                                                                                                                  USA
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                    US/08/413,708B
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Pred. No.
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Query Match
Best Local Similarity
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Best Local Similarity
"hehes 6; Conserv
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Search completed: April Job time: 79 sec
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US-09-192-048-24
                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 24
                                                                                                                                                                                                                                                                                                                              Patent No. 6063592
                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 24, Application US/09192048 Patent No. 6063592
                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/192,048
CURRENT FILING DATE: 1998-11-13
NUMBER OF SEQ ID NOS: 27
                                                                                                                                                                                                                                                                                                                                        APPLICANT: Lee, Soohee
TITLE OF INVENTION: Kell Protein Proteolytic Activity
FILE REFERENCE: Sequence 1-27
                                                                                                                                                                                                                            LENGTH: 14
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 202-737-3528 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/207
FILING DATE: 09-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 105061
FILING DATE: 16-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS: LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 16-MAR-1994 ATTORNEY/AGENT INFORMATION:
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TOPOLOGY: li
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                                                                       6 FTDNYTRLR 14
                                                                                                 6 FNDVTTRLR 14
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                                                                                                                                          27.1%;
66.7%;
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Pred. No. 2.3e
0; Mismatches
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                                                                                                                                          Score 26; DB 3;
Pred. No. 2.3e+02;
                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .3e+02;
                                                                                                                             3; Indels
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OM protein - protein search, using sw model

Run on:

January 6, 2002, 09:09:12; Search time 19.6 Seconds (without alignments) 104.934 Million cell updates/sec

Title:
Perfect score:
Sequence: US-09-020-393B-18 145

1 KCLGYHLDVSLAFSEISVGAEFNKDDC 27

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 5455

Minimum DB seq length: 0 Maximum DB seq length: 27

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	80	. 7	6	v	4	ω	2	1	No.	Result
23	23	23	23	23	23	23	23	24	24	24	24	24	24	25	25	26	26	26	26	26	26	26.5	27	27	28	28	28	31	Score	
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pyrrologuinoline q	major milk gland p hypothetical prote	outer layer protei	cartilage oligomer	buccalin - Califor	probable photosyst	brain natriuretic	annexin V - rat (f	gamma-glutamyl tra	CDK inhibitor - mo	cytochrome-c oxida	pyrroloquinoline q	natriuretic peptid	brain natriuretic	Ca2+-transporting

ALIGNMENTS

RESULT 2 A60889 A60889 Clactory glycoprotein RB-8 - rat (fragment) C;Species: Rattus norvegicus (Norway rat) C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999 C;Accession: A60889 R;Schwob, J.E; Gottlieb, D.I. R;Schwob, J.E; Gottlieb, D.I. J. Neurosci. 8, 3470-3480, 1988 A;Title: Purification and characterization of an antigen that is spatially segregated A;Reference number: A60889; MUID:89010968 A;Accession: A60889; MUID:89010968 A;Accession	
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Query Match 19.3%; Score 28; DB 2; Length 17; Best Local Similarity 54.5%; Pred. No. 5.5e+02; Matches 6; Conservative 3; Mismatches 2; Indels

0;

Gaps

0,

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ribosomal protein L30 - Nocardia asteroides (fragment)
C;Species: Nocardia asteroides
C;Date: 10-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 28-Oct-1994
C;Accession: JP006
R;Ochi, K.
submitted to JIPID, February 1994
A;Description: Phylogenetic diversity in the genus Bacillus and comparative A;Accession: JP0066
A;Accession: JP0066
                                               A:Molecule type: protein
A:Residues: 1-22 <OCH>
C:KeywOrds: protein biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 3
A36399
C-type natriuretic peptide - frog
C:Species: Ranidae gen. sp. (frog)
C:Date: 01-Feb-1991 #sequence_revisi
C:Accession: A36399
C:Caccesion: A36399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Barber, D.L.; Sanders, E.J.; Aebersold, R.; Schneider, W.J.
J. Biol. Chem. 266, 18761-18770, 1991
A;Title: The receptor for yolk lipoprotein deposition in the A;Reference number: A41006; MUID:92011638
A;Accession: A41006
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-27 <BAR>
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Best Local Similarity
"~+~hes 7; Conserv:
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C;Species: Gallus gallus (chicken)
C;Date: 12-Jun-1992 #sequence_revision 12-Jun-1992 #text_change 23-Mar-1993
C;Accession: A41006
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A;Title: Isolation and sequence determination of frog C-type natriuretic peptide. A;Reference number: A36399; MUID:91083642
A;Accession: A36399
A;Status: preliminary
A;Status: preliminary
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A:Residues: 1-22 <YOS>
C:Superfamily: natriuretic peptide A precursor
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epidermal growth
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factor,

high molecular weight -

rat (fragment)

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A; Note: this protein was identified as biliverdin reductase; the identification is quenches, M.D.; Polevoda, B.V.; Huang, T.J.; McCoubrey Jr., W.K.

Eur. J. Biochem. 235, 372-381, 1996
A; Title: Human biliverdin IX-alpha reductase is a zinc-metalloprotein. Characterizati A; Reference number: S62622; MUID:96202961
                                                                                                                                               A;Molecule type: protein
A;Residues: 1-20 <MAW>
C;Superfamily: protein kinase C inhibitor; histidine (
C;Keywords: homodimer; protein kinase inhibitor; zinc
                                                                                                                                                                                                                                                                                                                                                                  protein kinase C inhibitor - human (fragment)
N;Alternate names: histidine triad nucleotide-binding protein
C;Species: Homo sapiens (man)
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C;Accession: $72501; $62623
R;Maines, M.D.; Trakshel, G.M.
Arch. Biochem, Blophys. 300, 320-326, 1993
A;Title: Purification and characterization of human biliverdin reductase.
A;Recession: $72501
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Thes 4; Conserv:
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A;Residues: 1-25 <ROM>
C;Superfamily: L-lactate dehydrogenase
C;Keywords: oxidoreductase; tricarboxylic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, NOMEMBEL, T.O.; Hund, H.K.; Speth, A.R.; Lingens, F. Biol. Chem. Hoppe-Seyler 370, 763-768, 1989
A;Title: Purification and N-terminal amino-acid sequence number: S04956; MUID:89374824
A;Accession: S07574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       malate dehydrogenase (EC 1.1.1.37) - Phenylobacterium immobile (fragment) C;Species: Phenylobacterium immobile C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 02-Aug-1994 C;Roccession: S07574 R;Rommel, T.O.; Hund, H.K.; Speth, A.R.; Lingens, F.
                                                                                       Query Match
Best Local :
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Pred. No. 1e+03;
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C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_c
C:Accession: S08301
R:Nexo, E.; Jorgensen, P.E.; Thim, L.; Roepstorff, P.
Biochim. Biophys. Acta 1037, 388-393, 1990
A;Title: Purification and characterization of a low and a A;Reference number: S08288; MUID:90181442
A;Accession: S08301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Umezawa, Y.; Kuge, S.; Kikyo, N.; Shirai, T.; Watanabe, J.; Fujiwara, M.; Okabe, T. Jpn. J. Clin. Oncol. 21, 251-255, 1991
A;Title: Identity of brain-associated small cell lung cancer antigen and the CD56 (NKH-: A;Reference number: A61392; MUID:92046737
A;Accession: A61392
                                                                                                                                                                                                                                                   Biochemistry 23, 6210-5216, 1984
A;Title: Construction of DNA sequences complementary
A;Reference number: I52392; MUID:85122694
A;Accession: I65270
                                                                                                                                                                                                                                                                                                                                                               collagen alpha 1(I) chain - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 13-Aug-1999
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                                                       Query Match
Best Local Similarity
"hes 5; Conserv
                                                                                                                                                                                                                                                                                                           R; Genovese, C.; Rowe, D.; Kream, B.
Biochemistry 23, 6210-6216, 1984
                                                                                                                                                                                                                                                                                                                                               C; Accession:
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A; Residues: 1-18 <UME>
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A; Residues: 1-21 < RES>
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                                                                                                                                                                                                                                    A; Status: preliminary; translated
                                                                                                                                                             Cross-references: GB:M12200; NID:g203191; PIDN:AAA40835.1; Superfamily: collagen alpha 2(I) chain; fibrillar collagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Species: Homo sapiens (man)
Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 09-Sep-1994;
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21
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Pred. No.
                                                                 Score 26; DB 2; LC
Pred. No. 1.4e+03;
""cmatches 7;
                                                                                                                                                                                                                                    from GB/EMBL/DDBJ
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Pred. No. 1.2e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-Jun-1992 #text_change 30-Sep-1993
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1e+03;
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A48810
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fibrinogen B beta subunit - African clawed frog (fragment) C:Species: Xenopus laevis (African clawed frog) C:Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_c
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A;Description: Cloning of a chitinase homolog which lacks chitin bin A;Reference number: Z23105
A;Accession: T46622
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein c1 - loblolly pine
C;Species: Pinus taeda (loblolly pine)
C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 18-Feb-2000
C;Accession: T46622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pyrrologuinoline quinone precursor - Acinetobacter calcoaceticus N;Alternate names: pqq gene IV protein C;Species: Acinetobacter calcoaceticus C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      \label{eq:final_final_final} F; 16, 20/Product: pyrroloquinoline quinone *status F; 16-20/Cross-link: pyrroloquinoline quinone (Glu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: pqqA
C;Superfamily: pyrrologuinoline quinone precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:X06452; NID:g38740; PID:g130796
A;Note: this ORF is not annotated in GenBank entry ACPR
R;Goosen, N.; Hulimen, R.G.; van de Putte, P.
J. Bacteriol. 174, 1426-1427, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:U31309; NID:g974285; PID:g974287
A;Experimental source: strain s6PT2xs6PT3; 8 month seedli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-24 < CHA>
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A; Residues: 1-24 <GOO>
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A;Accession: B32252
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Best Local Similarity 41.,
Thes 5; Conservative
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Best Local
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Local Similarity 40.0%;
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nk: pyrroloquinoline quinone (Glu, Tyr) #status predicted
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41.7%;
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Pred. No. 1.6e+03;
"""" tches 2;
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Pred. No. 1.6e+03;
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     #text_change 21-Jul-2000
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apolipophorin III - house cricket (fragment)
C;Species: Acheta domesticus (house cricket)
C;Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_ch
C;Accession: A60295
R;Strobel, L.M.; Kanost, M.R.; Ziegler, R.; Wells, M.A.
Insect Biochem. 20, 859-863, 1990
A;Title: Adipokinetic hormone causes formation of a low den
A;Reference number: A60295
A;Accession: A60295
A;Molecule type: protein
A;Residues: 1-20 <STR>
C.Comment: This monatai
                                                                                                                                                                                                                            Complement receptor - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 12-Aug-1996 *sequence_revision 12-Aug-1996 *text_change 21-Jul-2000
C;Accession: 137261
C;Accession: 137261
C;Accession: 137261
C;Accession: 137261
C;Accession: 137261
C;Accession: 137261; MUID:93018869
A;Reference number: 137261; MUID:93018869
A;Accession: 137261
A;Ac
                                                                                                                                          A;Cross-references:
A;Map position: 1q32
                                                                                                                                                                                                               C; Genetics:
                                                                                                                                                                                      A; Gene: GDB:CR2
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R;Roberts, L.R.; Nichols, L.A.; Holland, L.J.
Biochemistry 32, 11627-11637, 1993
A;Title: Transcriptional regulation of the Xenopus laevis B beta fibrinogen subunit A;Reference number: A48810; MUID:94032285
A;Accession: A48810
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Matches
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A; Residues: 1-25 < ROB>
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4 TTGADEN 10
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                        4;
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33.3%;
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57.1%;
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23.5%;
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       Score 25; DB
Pred. No. 2.7e
4; Mismatches
              4;
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m NCBI backbone (NCBIN:138880, NCBIP:138881)
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Pred. No. 1.9e
2; Mismatches
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A; Residues:
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RESULT 18
$38739
Lipid transfer protein $2 - spinach (fragment)
C;Species: Spinacia oleracea (spinach)
C;Date: 08-Jun-1994 #sequence_revision 19-Jan-1996 #text_change 03-May-1996
C;Accession: $38739
                                                                                                                                                                                                                                                                                                                                           C;Date: 19-Apr-1991 #sequence_revision 19-Apr-1991 #text_change 18-Jun-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 es of damage
C;Superfamily: glutathione transferase
C;Keywords: dimer; transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Description: catalyzes the nucleophilic conjugation of intracellular glutathione A;Pathway: detoxification; xenobiotics metabolism A;Note: increased hydrophilicity of GSH-conjugates facilitates their further metabolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: protein
A; Residues: 1-17 < ROU>
A; Experimental source: liver; cytosolic
C; Comment: At least five species-independent classes of cytosolic
s mitochondrial form are known.
C; Complex: dimer
C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     glutathione transferase (EC 2.5.1.18) class alpha 6a - pig (fragment) N;Alternate names: glutathione S-transferase class alpha 6a C;Species: Sus scrofa domestica (domestic pig) C;Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-May-1999 C;Accession: S71864 R;Rouimi, P.; Anglade, P.; Debrauwer, L.; Tulliez, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biochem. J. 317, 879-884, 1996
A;Title: Characterization of pig liver glutathione
A;Reference number: S71864; MUID:96332484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Reference number: A;Accession: S71864
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60.0%;
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35.7%;
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Pred. No. 2.3e+03;
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Pred. No. 2
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formaldehyde dehydrogenase (glutathione) (EC 1.2.1.1) class III low activity form - C;Species: Gadus morhua (Atlantic cod)
C;Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 20-Mar-1996
C;Accession: C46285
R;Danielsson, O; Jornvall, H.
                                                                                                                                                                                                                                                            R;Van den Broek, P.J.A.; Van Leeuwen, C.C.M.; Weusthuis, R.A.; Postma, E.; Van Dijken, Blochem. Blophys. Res. Commun. 200, 45-51, 1994
A;Title: Identification of the maltose transport protein of Saccharomyces cerevisiae. A;Reference number: PC2133; MUID:94220124
A;Accession: PC2134
                                                                                                                                                                                                                                                                                                                                                        maltose transport protein - yeast (Saccharomyces cerevisiae) (fragment)
C;Species: Saccharomyces cerevisiae
C;Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 07-May-1999
C;Accession: PC2134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Note: sequence extracted from NCBI backbone (NCBIP:116269)
C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase
C;Keywords: NAD; oxidoreductase
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                                                                                                                                                                             C; Superfamil
C; Keywords:
                                                                                                                                                                                          A; Experimental source: plasma membrane C; Superfamily: maltose transport protein
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A;Molecule type: protein
A;Residues: 1-22 <DAN>
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Proc. Natl. Acad. Sci. U.S.A. 89, 9247-9251, 1992
A; Title: "Enzymogenesis": classical liver alcohol
A; Reference number: A46285; MUID:93028441
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A;Residues: 1-21 <SEG>
C;Superfamily: phospholipid transfer protein
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A; Accession: S38739
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A;Title: Purification and antipathogenic ac
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14 CIGY 17
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les 5; Conserv
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pred. No. 3.1e+03;
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Pred. No. 3.1e+03;
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Pred. No. 2.9e+03;
1; Mismatches 0
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                                                                                                                                                                           A;Status: preliminary
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Matches 5
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Best Local Similarity
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14 CIGY 17
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nes 5; Conserv
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3 GFKLDVT 9
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C;Accession: B61597
R;Shimeno, H.; Toda, A.; Ogata, S.; Nagamatsu, A. Drug Metab. Dispos. 19, 291-297, 1991
A;Title: Purification and aminopyrine monooxygenase A;Reference number: A61597; MUID:91292910
A;Accession: B61597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: PS0371
R;Rhiel, E.; Stirewalt, V.L.; Gasparich, G.E. Gene 112, 123-128, 1992
A;Title: The psaC genes of Synechococcus sp. A;Reference number: JS0694; MUID:92201692
A;Accession: PS0371
                                                                                                                                                                                                                                                                                          cytochrome P450 AL-2 - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995
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$38738
Lipid transfer protein S1 - spinach (fragment)
C; Species: Spinacia oleracea (spinach)
C; Species: Spinacia (spinach)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-14 <RHI>
A;Cross-references: GB:M86238; NID:g154574; PIDN:AAA27351.1; PID:g552030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Synechococcus sp.
C;Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEBS Lett. 332, 243-246, 1993
A; Title: Purification and antipathogenic activity
A; Reference number: S38736; MUID:94009709
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PS0371
hypothetical protein (psaC region) - Synechococcus sp. (fragment)
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Generative
    Conservative
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75.0%;
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57.1%;
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Pred. No. 2.7e+03;
2; Mismatches 1
Score 23; DB 2; Le
Pred. No. 2.7e+03;
4; Mismatches 4;
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Pred. No. 3.2e+03;
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                                         Length 14;
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Search completed: January 6, 2002, 09:13:53 Job time: 281 sec
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A;Molecule type: protein
A;Residues: 1-15 <CHA>
C;Keywords: heme; salivary gland; vasodilator
                                                                                                                                                                                                                                                                                                                                                                        N;Alternate names: nitric oxide-carry protein NP4
C;Species: Rhodnius prolixus
C;Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 17-Mar-1999
C;Accession: D563B5
R;Champagne, D.E.; Nussenzveig, R.H.; Ribeiro, J.M.C.
J. Biol. Chem. 270, 8691-8695, 1995
A;Title: Purification, partial characterization, and cloning of nitric oxide-carrying he
A;Accession: D563B5
A;Cession: D563B5
MUID:9523B361
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R;Chow, L.P.; Fukaya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JIPID, October 1994
A;Description: Two dimensional polyacrylamide gel electropheresis of Fusarium sporotrich A;Reference number: PA0051
A;Accession: PA0062
A;Rolecule type: Protein
A;Residues: 1-15 CCHO>
C;Keywords: carbon-oxygen lyase; hydro-lyase
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Thehes 5; Conserve
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                                                                                                                                                                         Query Match 15.9%; Score 23; DB 2; La Best Local Similarity 100.0%; Pred. No. 2.9e+03; Matches 4; Conservative 0; Mismatches 0;
                                                                                                    12 FNKD 15
                                                                                                                                              22 FNKD 25
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71.4%; Pred. No. 2.9e+03;
^. Mismatches 2;
                                                                                                                                                                                                               Length 15;
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Perfect score:
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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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SP34_DICMU
NU4M_TRIRU
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PQQA_KLEPN
PETM_SKECO
CX7A_CONTE
TKL4_LOCMI
FIBA_SHEEP
VI01_VACCV
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FMK7_PSEAE
COXC_THUOB
PQQA_PSEFL
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PQQA_ACICA
TPX_CLOPA
RM12_YEAST
XYLA_STRVN
BP37_LEUMA
AGI_EUPMA
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Acinetobacter.

RESU PQQA AC DT DT DT DE OC	ДУ	Z m O	DR DR DR DR SQ				E P P P P P	RESU MDH_		
PAC	3 16	Query Mat Best Loca Matches	Inter Inter Inter Pfam; PROSI Oxido NON_T SEQUE	Biol.	STRAI MEDLI Romme "Puri dehyd	MDH. Phenyloba Bacteria, Phenyloba NCBI_Taxl [1] [1]	01-FEB- 01-FEB- 30-MAY- 30-MAY-			00000044444440000000000000000000000000
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S Rel Rel Rel Rel Ca	7 20	ilarity Conserva	Prop. PRO01252; Prop. IPR001236; Prop. IPR001236; , PF00056; ldh; 11 ITE: PS00068; MDH Dreductase; Trica PROCE 25 AA; 26	Hoppe-SI IC ACTIV ITY: BELL ; S07574	74824; Portion And Hon and Non and Non and Non and Non Ses from	MDH. Phenylobacterium immobile Bacteria; Proteobacteria; Phenylobacterium. NCBI_TaxID=21; [1] SEQUENCE.	1991 (Rel. 17, -1991 (Rel. 17, -2000 (Rel. 39, DEHYDROGENASE (STANDARD		13.8 113.8 113.4 113.1 113.1 113.1 113.1 113.1 113.1 113.1
TANDARD; 23, Creat 23, Last 34, Last THESIS PROT 1coaceticus bacteria; 9		18.6 80.0 tive	w. w. d. d. d. d. m. m. m. m. m. m	eyler : ITY: L: ONGS TO	ubMed=; K., % -termin six ac	mobile teria;	Cre Las Las EC	DARD;		25 27 27 10 12 14 15 16 16
PRT; 24 AA. ed) sequence update) annotation update) EIN A (COENZYME PQ		%; Score 27; DB 1; %; Pred. No. 6.4e+02 1; Mismatches	NAD.	. 3	STRAIN=E; MEDLINE-89374824; PubMed-2775496; MEDLINE-89374824; PubMed-2775496; Rommel T.O., Hund HK., Speth A.R., Lingens F., Purification and N-terminal amino-acid sequence "Purification and N-terminal amino-acid sequence dehydrogenases from six actinomycetales strains Phenylobacterium immohlle strain E.":	on;	ated) t sequence update) t annotation update) 1.1.1.37) (FRAGMENT).	PRT; 25 AA.	ALIGNMENTS	GBX1_MOUSE DBH1_BIFLO BTX_ATRBI RL22_HALCU TRRSU TRRSU V25K_WSSV MAST_POLJA PH2_PERAM LE06_BIOGL RIPK_TRIKI PH3_PERAM PH4_PERAM PH4_PERAM
Q SYNTHESIS PROTEIN IV). Moraxellaceae;		Length 25; ; 0; Indels 0; Gaps 0	CRC64;	OXALOACETATE + NADH. MDH SUBFAMILY.	es of bacterial malate	Caulobacter group;				P82976 mus musculu P17615 bifidobacte P80163 atractaspis P05973 halobacteri P81740 leucophaea P82004 white spot P01517 polistes ja P82695 periplaneta P80745 biomphalari P16093 trichosanth P82696 periplaneta P82697 periplaneta

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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TPX_CLOPA STANDARD; PRT; 20 AA. P81361; P81361; Standard; PRT; 20 AA. 15-UL-1998 (Rel. 36, Created) 15-UL-1998 (Rel. 36, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) PROBABLE THIOL PEROXIDASE (EC 1.11.1.1.-) (CP 42) (FRAGMENT).
                                                                                                                                                                                                                           -1- SIMILARITY: BELONGS TO TO
                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=98291870; PubMed=9629918;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=1501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clostridium pasteurianum.
Bacteria; Firmicutes; Bac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"ACINETODACTER CALCOACETICUS genes involved in biosynthesis of the
COENTYME PYRTOLO-QUINOLINE, nucleotide sequence and
J. Bacteriol. 171:447-455(1989).

-!- FUNCTION: REQUIRED FOR CONNYME PYRROLO-QUINOLINE-QUINONE (PQQ)
BIOSYNTHESIS. THIS PROTEIN COULD FUNCTION AS A TEMPLATE FOR PQQ
ARE NECESSARY FOR THE SYNTHESIS.

ARE NECESSARY FOR THE SYNTHESIS.
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the Euro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way by non-profit institutions as long as its content is in no way.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: TO OTHER BACTERIAL POOA.
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       Similarity
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                                                                                                                                                                                                     BELONGS TO THE AHPC/TSA FAMILY. TPX SUBFAMILY
                                                                                                                                                                    TPX; PARTIAL
                                                                                                   2193 MW;
       17.28;
41.78;
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40.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillus/Clostridium group; Clostridiaceae;
    Score 25;
Pred. No.
                                                                                         08178FCD2782E765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4;
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DB 1;
1e+03;
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RESULT 5
XYLA_STRVN
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                   -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
-!- SIMILARITY: BELONGS TO THE XYLOSE ISOMERAS HSSP; P37031; LDXI.
InterPro; IPR001998; Xylose_isom.
PROSITE; PS00172; XYLOSE_ISOMERASE_1; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                      MEDLINE=90104230; PubMed=2604694; Vangrysperre W., Ampe C., Kersters-Hilderson H., Tempst P.; "Single active-site histidine in D-xylose isomerase from St violaceoruber. Identification by chemical derivatization an
                                                                                                                                                                                                                  01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence up
15-JUL-1990 (Rel. 38, Last annotation
XYLOSE ISOMERASE (EC 5.3.1.5) (FRAGMEN
Streptomyces violaceoruber
                                                                                                                                                         STRAIN=LMG 7183;
                                                                                                                                                                                       Bacteria, Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; St
NCHI_TaxID=1935;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RM12_YEAST STAN
P36522;
01-JUN-1994 (Rel. 2
01-JUN-1994 (Rel. 2
01-JUN-1994 (Rel. 2
MITOCHONDRIAL 60S R
                                                                                                                                                                                                              Bacteria;
                                                                                                                                                                                                                                                                          P14405
                                                                                                                                                                                                                                                                                   XYLA_STRVN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Extended N-terminal sequencing of proteins of the large ribosomal subunit from yeast mitochondria."; FEBS Lett. 284:51-56(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                          Ribosomal protein; Mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Grohmann L., Graack H.-R., Kruft V., Kitakawa M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      _YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomycetales;
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast).
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4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29, Created)
29, Last sequence update)
29, Last sequence update)
29, Last annotation update)
RIBOSOMAL PROTEIN L12 (YML12) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                               1851 MW;
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36.4%;
                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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Pred.
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                                                                                                                                                                                      Streptomycetaceae; Streptomyces.
                                                                             D-XYLULOSE
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No.
                                 ISOMERASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Choli T.,
                                                                                                                                                                                                                                                                               12 AA
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                                                                 THE ACTIVITY
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                                                                                                                Streptomyces
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01-FEB-1994 (Rel. 2
01-FEB-1994 (Rel. 2
LECTIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                isoforms.";
isoforms.";
peptides 18:7-15(1997).
-:- TISSUE SPECIFICITY: BRAIN.
-:- MASS SPECTROMETRY: MW=1435.7; METHOD=MALDI.
-:- MASS SPECTROMETRY: MW=1435.7; METHOD=MALDI.
--- SPOUENCE 13 AA; 1436 MW; 8E532C9DE9A7D1B5
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Me
Pterygota; Ne
Blaberoidea;
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P33888;
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NON_TER
SEQUENCE
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30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence up
20-AUG-2001 (Rel. 40, Last annotation
BRAIN PROTEIN 37F3.
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TISSUE-Latex;
MEDLINE-93357266; PubMed-8353129;
MEDLINE-93357266; PubMed-8353129;
Stirpe F., Licastro F., Morini M.C., Parente A., Savino Abbondanza A., Bolognesi A., Falasca A.I., Rossi C.A.;
"Purification and partial characterization of a mitogeni
                                                                              Euphorbia characias (Spurge).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheop Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheop Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; eurosids I; Malpighiales; Euphorbiaceae; Euphorbia.
                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=97269266; PubMed=9114447;
Muren J.E., Naessel D.R.;
"Seven tachykinin-related peptides isolated from the brain madeira cockroach; evidence for tissue-specific expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LEUMA
                                                     SEQUENCE.
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                                                                        NCBI_TaxID=3991;
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nes 4; Conser
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28, Last annotation update)
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1375
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55.6%;
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Pred. No. 1.4e+03;
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FMK7_PSEAE
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DT 15-JUL-1998 (
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ID ANEC CHICK
AC P21805;
DT 01-MAY-1991
DT 20-AUG-2001
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NON_TER
SEQUENCE
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SEQUENCE
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-- FUNCTION: VASORELAXANT ACTIVITY. HAS A CGMP:
-- SUBCELLULAR LOCATION: SECRETED.
-- SIMLLARITY: BELONGS TO THE NATRIURETIC PEPTIPIR; JT0581; JT0581.
                                                                                                                                                                                                                                                                                                                                                             MEDLINE=91113186; PubMed=1989595; Arimura J.J., Minamino N., Kangawa K., Matsuo H.; Isolation and identification of C-type natriuretic chicken brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C-TYPE NATRIURETIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     latex of Euphorbia marginata.";
Chim. Biophys. Acta 1158:33-9(1993).
FUNCTION: LECTIN THAT BINDS GALACTOSE, GALACTOSE-CONTAINING SUGARS
AND GENTIOBIOSE. IT IS STRONGLY MITOGENIC FOR HUMAN T LYMPHOCYTES.
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                                                                                                                                            Similarity 57... 4; Conservative
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Neognathae; Galliformes; Phasianidae; Phasianinae;
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66.7%;
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57
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annotation
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Pred. No. 1.9e
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Pred. No. 2.3e+03
0; Mismatches
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1.9e+03;
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(Rel.

36, Created)
36, Last sequence update)

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RESULT 10
COXC_THOME
ID COXC_T
AC P80973
DT 01-NOV
DT 01-NOV
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OS %hannu,
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                                       CONC_THUOB STANDARD; PRT; P80973; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence up 30-MAY-2000 (Rel. 39, Last annotation CYTOCHROME C OXIDASE DELYPEPTIDE VA-2
                  Thunnus obesus (Bigeye tuna).
Eukaryota; Metazoa; Chordata; Craniata;
          Actinopterygii;
                                                                                                                                                                                                                                                                                                                             NON_TER
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-56/10702; PubMed-8845350;
Campbell A.P., McInnes C., Hodges R.S., Sykes B.D.;
Campbell A.P., McInnes C., Hodges R.S., Sykes B.D.;
"Comparison of NMR solution structures of the receptor binding domains of Pseudomonas aeruginosa pili strains PAO, KB7, and PAK; implications for receptor binding and synthetic vaccine design.";
Biochemistry 34:16255-16268(1995).

1- SUBUNIT: THE PILI ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4
NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL CONSISTORY BELONGS TO THE N-ME-PHE PILI FAMILY.
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PROSITE; PS00409; PROKAR_NTER_METHYL; PARTIAL Fimbria; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; S67809; CAB32861.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                      Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "A multicenter comparison of methods for typing strains of pseudomonas aeruginosa predominantly from patients with cyfibrosis. The International Pseudomonas aeruginosa Typing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=94103636; PubMed=7903973;
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FIMBRIAL PROTEIN
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1KB8; 29-JAN-96.
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                                                                                                                                                                                                                                                       Similarity 4; Conserv
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                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dis. 169:134-142(1994).
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AA;
       Neopterygii; Teleostei;
                                                                                                                                                                                                                           27
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Pred. No. 2.4e
3; Mismatches
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                                             update)
(EC 1.9.
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   Euteleostei;
            Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                              DB 1;
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Neoteleostei;
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PQQA_PSEFL
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                                                                                                            the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
              SEQUENCE
                                             EMBL; X87299; CAA60732.1; -.
EMBL; X87299; CAA60731.1; ALT_INIT.
                                                                                                                                                                                                                                                                This
                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-96064397; PubMed-8526497; Schnider U., Keel C., Defago G., Haas D.; "Tn5-directed cloning of pqq genes from Pseudomonas fluorescens mutational inactivation of the genes results in overproduction antibiotic pyoluteorin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1996 (
01-OCT-1996 (
01-OCT-1996 (
COENZYME PQQ
                                                                                                                                                                                                                                        between the
                                                                                                                                                                                                                                                                                                                                                            Appl. Environ. Microbiol. 61:3856-3864(1995).
-!- FUNCTION: REQUIRED FOR COENZYME PYRROLO-QUINOLINE-QUINONE BIOSYNTHESIS. THIS PROTEIN COULD FUNCTION AS A TEMPLATE FO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LUIT. J. Blochem. 248:99-103(1997).

-!- FUNCTION: THIS IS THE HEME A-CONTAINING CHAIN OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN MITOCHONDRIAL ELECTRON TRANSPORT.
-!- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4 FERRICYTOCHROME C.
-!- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE.
-!- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE.
-!- SIMILARITY: BELLONGS TO THE CYTOCHROME C OXIDASE VA FAMILY.
OXIOCREDUCTS: Heme; Mitochondrion; Inner membrane.

NON_TER 24
SEQUENCE 7. 1.
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P55171;
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SEQUENCE
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MEDLINE=97454291; PubMed=9310366;
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Kadenbach B.;
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NCBI_TaxID=8241;
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Q SYNTHESIS PROTEIN A.
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ED13A879B2EA3E8E CRC64;
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SEQUENCE
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01-JUN-1994
01-NOV-1997
                                                                                                       TISSUB-Egg yolk;
MEDLINE-92392273; PubMed=1520265;
Kido S., Morimoto A., Kim F., Doi Y.;
"Isolation of a novel protein from th
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P80326;
                                   DISULFIDE BONDS.
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SEQUENCE 20 AA; 2
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Martin C., Leis W., Radler F.;
J. Gen. Appl. Microbiol. 40:0-0(1994).
-!- SUBCELLULAR LOCATION: SECRETED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomycetales;
NCBI_TaxID=36015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pichia kluyveri (Yeast).
Eukaryota; Fungi; Ascomycota;
                                                                                       memorane.";
Biochem. J. 286:17-22(1992)
                                                                                                membrane.
                                                                                                                                              SEQUENCE
                                                                                                                                                                                           Gallus gallus (Chicken)
Eukaryota; Metazoa; Cho
                                                                                                                                                                                                            VITELLINE MEMBRANE OUTER LAYER PROTEIN
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20-AUG-2001 (Rel.
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Neognathae; Galliformes; Phasianidae;
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RESULT 15
PQQA_KLEPN
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AC P27503;
DT 01-AUG-1992 (1)
DT 01-OCT-1996 (1)
DE COENZYME PQQ (1)
GN PQQA.
OS Klebsiella pno
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01-NOV-1995
20-AUG-2001
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Gnehm C.L., McDonald L.A.,
Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro: IPR001109; HupF_HypC.
PROSITE; PS01097; HuPF_HYPC; UNKNOWN_1.
Hypothetical protein; Complete proteome.
SEQUENCE 21 AA; 2387 MW; 2A63C08B47C2ED3B CRC64;
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Science 269:496-512(1995).
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Bacteria; Proteobacteria;
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P45194;
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  Proteobacteria;
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                           pneumoniae
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2Q SYNTHESIS
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PROTEIN HI1390.
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S PROTEIN A.
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Pred. No. 3
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Best Local Similarity
"~+~hes 4; Conserv
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Tada N., Otsuka S., Oyaizu H., Matsumoto S.;

Tlastid DNA sequences of Skeletonema costatum NIES 323.

Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.

-!- FUNCTION: CYTOCHROME B6-F COMPLEX SUBNIT.

-!- FUNCTION: THYLAKOID MEMBRANE-ASSOCIATED
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                                                     This SWISS-PROT entry is copyright. It is produced through a chetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is
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096810;
20-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; stramenopiles; Bacillariophyta; Coscinodiscophyceae; Thalassiosirophycidae; Thalassiosirales; Skeletonemataceae;
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20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
CYTOCHROME B6-F COMPLEX SUBUNIT VII (CYTOCHROME B6F COMPLEX SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=2843;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Skeletonema
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PETM OR YCF31.
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Mol. Gen.
-!- FUNCTI
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MEDLINE=92212293; PubMed=1313537;
Meulenberg J.J.M., Sellink E., Riegman N.H., Postma P.W.;
"Nucleotide sequence and structure of the Klebsiella pneur
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NCBI_TaxID=573;
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                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE PETM FAMILY
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FUNCTION: REQUIRED FOR COENZYME PYRROLO-QUINOLINE-QUINONE (PQO)
BIOSYNPHESIS. THIS PROTEIN COULD FUNCTION AS A TEMPLATE FOR PQO
SYNTHESIS AND PROVIDE THE GLUTAMATE AND TYROSINE RESIDUES WHICH
ARE NECESSARY FOR THE SYNTHESIS.
SIMILARITY: TO OTHER BACTERIAL PQOA.
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40.0%;
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Pred. No. 3.5e+03;
Pred. No. 3.5e+03;
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DT CONOTO.
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TKL4_LOCMI
ID TKL4_L
AC P30250
DT 01-APR
DT 01-APR
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                                                                                                                                                                  Query Match
Best Local S
Matches 7
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       TKL4_LOCMI
P30250;
01-APR-1993
01-APR-1993
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Best Local
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MOD_RES
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                           Nakamura T., Yu 2., Fainzilber M., Burlingame A.L.;

"Mass spectrometric-based revision of the structure of
peptide toxin with gamma-carboxyglutamic acid, TxVIIA,
snail, Conus textile.";

Protein Sci. 5:524-530(1996).

1. FUNCTION: POTENT NEUROTOXIN. MAY EXERT ITS EFFECTS
OF THE NEUROMUSCULAR JUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-NEOVICARIUS; TISSUE-Venom; MEDLINE-92104183; PubMed-1761058; Fainzilber M., Gordon D., Hasson A., "Mollusc-specific toxins from the ver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CX7A_CONTE STANDARD; PRT; 27 AA.

P24150;
P24150;
01-MAR-1992 (Rel. 21, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
CONOTOXIN TXVIIA (TXXIIA).
Conus textile (Cloth-of-gold cone).
Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97022130; PubMed=8868490;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eur. J. Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                            REVISIONS TO 1 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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NON_TER 1
TRANSMEM 2
SEQUENCE 25 A
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                                                                                                                                                                                                                                                                                                     !- PTM: THREE DISULFIDE BONDS ARE PRESENT.
!- MASS SPECTROMETRY: MW=3088.9; METHOD=ELECTROSPRAY.
                                                                                                               Н
                                                                                                                                   2 CLGYHLDVSLAFSEISVGAEFNKDDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 LSLGFALLKVQGE
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                                                                                                            CGGYS-----
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                                                                                                                                                                                                                                                                                                S19620; S19620
                                                                                                                                                                                                                                                                    Neurotoxin;
                                                                                                                                                                Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AJ132266; CAA10631.1;
       (Rel.
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                                           STANDARD;
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2
AA;
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25, Created)
25, Last sequence
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                                                                                                                                                                                                                                                               Vitamin K; Gamma-carboxyglutamic acid; 9 GAMMA-CARBOXYGLUTAMIC ACID.
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                                                                                                                                                                         14.8%;
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38.5%;
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                                                                                                                                                         Score 21.5; D
Pred. No. 4.8e
3; Mismatches
                                                                                                                                                                                                                           D7A49781300FE1E7
                                                                                                                                                                                                                                                   GAMMA-CARBOXYGLUTAMIC
                                                                                                                                                                                                                                           AMIDATION
                                          PRT;
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Pred.
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99ECF1B6CA3113AA
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No.
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nom of Conus
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Best Local :
                                          Query Match
Best Local Similarity
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                              Matches
                                                                                                                                                                                                                                                      Blomback B., Blomback M., Grondahl N.J.;
"Studies on fibrinopeptides from mammals.";
Acta Chem. Scand. 19:1789-1791(1965).
-I- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS POLYMERIZE. INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
                                                                                                                             HSSP;
Blood
                                                                                                                                                                                                                                                                                                                                                             Ovis aries (Sheep), and Capra hircus (Goat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovoidea; Caprinae; Ovis.
NCBI_TaxID-9940, 9925;
                                                                                                                                                                                                                                                                                                                                                                                                                                               P14451;
01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence up
01-MAY-1991 (Rel. 18, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Locustatachykinin III and IV: two additional insect neuropeptides with homology to peptides of the vertebrate tachykinin family."; Regul. Pept. 31:199-212(1990).
-i- FUNCTION: MYOACTIVE PEPTIDE. STIMULATES THE CONTRACTION OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schoofs L., Holman de Loof A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Locusta migratoria (Migratory locust).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;
Acridomorpha; Acridoidea; Acrididae; Locusta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1995 (Rel. 32, Last annotation update) LOCUSTATACHYKININ IV (TK-IV).
                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                       FIBRINOPEPTIDE A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FIBA_SHEEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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MOD_RES 10 10 AMIDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OVIDUCT AND FOREGUT.
-!- SIMILARITY: SOME SIMILARITY TO
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MEDLINE=91219696; PubMed=2132575;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=7004;
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nes 3; Conserv
 18 VGAEF
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                                                                                                                                                       AGGREGATION.

SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS (ALPHA, BETA, & GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS. MISCELLANEOUS: CONVERSION OF FIBRINGGEN TO FIBRIN IS TRIGGERED BY THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LGFH
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                                                                                                                               coagulation; Plasma.
                                                                                                                                              P02671; 1BBR.
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                              Conservative
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                                                                                                   AA;
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                                                                                                   1848
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75.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence update)
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Pred. No. 2.1e+03;
                                           Pred.
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                                                       Score 21;
                                                                                                   99C98873D1B059C5 CRC64;
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                              Mismatches
                                           No. 4
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                                                           DB 1;
                                           .1e+03;
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RESULT
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Matches 5; Conserv
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P16714;
01-AUG-1990
01-AUG-1990
01-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1995
01-FEB-1995
20-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RL10_KLEPN
P41190;
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                                                                                                                                       STRAIN-NCTC 5054;
Zhyvoloup A.N.;
Submitted (AUG-1993) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=88215015; PubMed=2835495;
Schmitt J.F.C., Stunnenberg H.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vaccinia virus (strain WR). Viruses; dsDNA viruses, no Orthopoxvirus.
                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Klebsiella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KLEPN
                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Virol. 62:1889-1897(1988)
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                                                                                                                                                                                                                                                                                                                                                                                         RPLJ
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2241 MW;
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Last sequence update)
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                                                                                                                                                                                                                                                                                                                                          gamma
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Pred. No. 4.3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6E97AA78D505C4B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    stage;
                                                                                                                                                                                                                                                                                                                                          subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Poxviridae;
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RESULT 23
CAMT_PINPS
ID &AMT_P
AC P81081
DT 15-JUL
                                                                                                                                       Matches
                                                                                                          Query Match
Best Local :
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P81081;
15-JUL-1998
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Q47608;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2001 (Rel. 39, Last seque
20-AUG-2001 (Rel. 40, Last annot
50% RIBOSOMAL PROTEIN LIO (FRAGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local
                                                                                                                                     Ribosomal protein.
INIT_MET 0
NON TER 23
SEQUENCE 23 AA;
                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                                                                   InterPro; IPR002363; Ribosomal_L10_
PROSITE; PS01109; RIBOSOMAL_L10; Pf
                                                                                                                                                                                   EMBL; X74444; CAA52455.1;
                                                                                                                                                                                                                                                                        Zhyvoloup A.;
Submitted (AUG-1993)
                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                  Bacteria; Pr
Enterobacter
                                                                   15
                                                                                                                                                                                                                                                                                                         NCBI_TaxID=550;
                                                                                                                                                                                                                                                                                                                                Enterobacter cloacae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X74445; CAA52456.1; -. PIR; S35975; S35975. PIR; S35976; S35976. InterPro; IPR002363; Ribosomal_L10_eub. PROSITE; PS01109; RIBOSOMAL_L10; PARTII
                                                                              14 SEISVGA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INIT_MET
                                                                                                       Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ribosomal protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                           14 SEISVGA 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                        mitted (AUG-1993) to the EMBL/GenBank/DDBJ databases.
SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.
                                                                 SEVAKGA
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      (Rel. 36, Created)
                                                                                              Conservative
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                       STANDARD;
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57.1%;
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                                                                                           Score 21; DB
Pred. No. 4.9e
2; Mismatches
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                      24
                                                                                                    DB 1;
4.9e+03
                                                                                                                                                                                                   (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                    update)
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4.7e+03;
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ACC CCC
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Query Match
Best Local :
      "Amino acid sequence and relative biological activity of eel atrial natriuretic peptide.";
Biochem. Biophys. Res. Commun. 164:537-543(1989).
-!- FUNCTION: EXHIBITS NATRIURETIC AND VASODEPRESSOR ACTIVITY. HAS ACCEMP-STIMULATING ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                            P18144;
01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ATRIAL NATRIURETIC FACTOR (ANF) (ATRIAL NATRIURETIC
                                                                                                                                                    MEDLINE=90026430;
Takei Y., Takahasl
                                                                                                                                                                                                                                                                                                   Anguilla japonica (Japanese eel).
Eukaryota; Metazoa; Chordata; Craniata;
Actinopterygi; Neopterygi; Teleostei;
Anguillidae; Anguilla.
NCBL_TaxID-7937;
                                                                                                                                                                                                       TISSUE=Heart atrium;
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Electrophoresis 20:1098-1108(1999)
-i- FUNCTION: INVOLVED IN THE REIN
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TISSUE-Meedle;
MEDLINE-98418576; PubMed-9747804;
Costa P., Bahrman N., Frigerio J.-M.,
Costa P., Bahrman N., Frigerio J.-M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=99274088; PubMed=10344291;
Costa P., Pionneau C., Bauw G., Dubos C.,
Frigerio J.-M., Plomion C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JUL-1998 (Rel. 36, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
PROBABLE CAFFEOYL-COA O-METHYLTRANSFERASE (EC 2.1.1.104) (TRANS-CAFFEOYL-COA 3-O-METHYLTRANSFERASE) (CCOAOMT) (CCOAOMT) (WATER STRESS PINUS PINU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Separation and characterization of needle and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Needle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE.
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nes 4; Conser
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CGMP-STIMULATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MISCELLANEOUS: ON THE L.
IS: 5.2, ITS MW IS: 30 KDA.
Tansferase; Methyltransferase.
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PATHWAY: LIGNIN BIOSYNTHESIS.
SUBUNIT: HOMODIMER (BY SIMILARITY).
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                                                                                                                                     Takahashi A., Watanabe T.X.,
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4 AA;
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                                                                                                                                                                       PubMed=2529857;
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2447
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GGER THE DISEASE F
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                                                                                                                                 Nakajima
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                                                                                                                                                                                                                                                                                                                                      Vertebrata; Euteleostomi;
Anguilliformes; Anguilloidei;
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5.1e+03
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RESULT 25
CD59_SHEEP
Query Match
Best Local Similarity
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AN MEDILIES-3239201; PubMed=7682985;

AN MEDILIES-3239201; PubMed=7682985;

AN AMEDILIES-3239201; PubMed=7682985;

AN Own den Berg C.W., Harrison R.A., Morgan B.P.;

AN Van den Berg C.W., Harrison R.A., Morgan B.P.;

AN Van den Berg C.W., Harrison R.A., Morgan B.P.;

AN Van den Berg C.W., Harrison R.A., Morgan B.P.;

AN Van den Berg C.W., Harrison R.A., Morgan B.P.;

AN Van den Berg C.W., Harrison R.D.

RT of its complement inhibitory activity.";

RI Inmunology 78:349-357,(1993).

CC -i- FUNCTION: POTENT INHIBITOR OF THE COMPLEMENT MEMBRANE ATTACK

CC COMPLEX (MAC) ACTION, ACTS BY BINDING, IN A SPECIES SPECIFIC

CC COMPLEX (MAC) ACTION, ACTS BY BINDING, IN A SPECIES SPECIFIC

CC COMPLEX (MAC) ACTION, ACTS BY BINDING, IN A SPECIES OF C9

CC COMPLEX (MAC) ACTION, ACTS BY BINDING, IN A SPECIES OF C9

CC MANNER, TO THE COMPLEMENTS OF THE MEMBRANE BY A GPI-ANCHOR.

CC -I- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR.

CC -I- TISSUE SPECIFICITY: EXPRESSED IN ERYTHROCYTES AND LYMPHOCYTES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                           Antigen; Glycoprotein.

NON_TER 1 1

DISULFID 3 25

DISULFID 6 12

CARBOHYD 17 17

UNSURE 3 3

UNSURE 6 6

UNSURE 17 17

UNSURE 17 17

UNSURE 18 18

UNSURE 25 25

NON_TER 27 27
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DISULFID
SEQUENCE 2
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DISULFID
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SEQUENCE
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P58020;
P58020;
20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
20-AUG-2001 (Rel. 40, Last annotation update)
CD59 GLYCOPROTEIN (MEMBRANE ATTACK COMPLEX INHIBITION FACTOR) (MACIF)
(MAC-INHIBITORY PROTEIN) (MAC-IP) (PROTECTIN) (COMPLEMENT INHIBITORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria; Ceta.
Bovidae; Caprinae; Ovis.
NCBI_TaxID=9940;
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InterPro; IPR000663; Natr_peptide.
Pfam; PF00212; ANP; 1.
                                                                                                                                                                                                                                                                                         NOT DETECTED IN PLATELETS.
PROSITE; PS00983; LY6_UPAR; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ovis aries (Sheep).
Eukaryota; Metazoa;
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-1- SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY
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27 AA; 2792 MW; 9EF5100CCF282B4D CRC64;
                  Conservative
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                                                                                                3025 MW;
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                              14.5%;
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               Score 21; DB 1;
Pred. No. 5.8e+03;
2; Mismatches 5
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Pred. No. 5.8e+03;
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Qy 18 VGAEFNKDDC 27: |:| |
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Search completed: January 6, 2002, 09:17:45
Job time: 278 sec
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Result
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Maximum DB seq length: 27
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Q913b4 gluconobact
Q913b4 gluconobact
Q941b2 caenorhabdi
Q41052 porphyra sp
Q94188 trypanosoma
Q94569 nitrosomona
Q9458 trypanosoma
Q82392 human t-cel
Q82410 human t-cel
Q82411 human t-cel
Q82411 human t-cel
Q82412 human t-cel
Q82412 human t-cel
Q82416 human t-cel
Q82416 human t-cel
Q82416 human t-cel
Q82417 human t-cel
Q82418 human t-cel
Q82567 plasmodium
Q9uc67 homo sapien
Q9454 helicobacte
Q9de23 gallus gall
Q63076 rattus norv
Q92574 phlabotomus
Q9z274 phlabotomus
Q9gi23 hepatitis c
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Q9prx2 struthio ca	Q9r591 bacillus th		080277 bacteriopha	hepatitis	037313 hepatitis c	Q9s8r3 brassica na	Q9ucd9 homo sapien	P92577 boa constri	Q9qv13 mus sp. col	Q9s8q6 spinacia ol	Q9s8q7 spinacia ol	Q9fac6 streptomyce	_	Q64973 alfalfa mos	Q9ucc9 homo sapien	Q91272 petromyzon	O37317 hepatitis c	homo sap	bovine	Q9quw9 rattus sp.	Q26089 polycelis n	_	Q61946 mus musculu	Q9r5s7 treponema d	092820 chimpanzee

ALIGNMENTS

RESULT Q9TWH2 ID Q AC Q DT 0 DT 0	Que Bes Mat Qy	RT R	RN OCC S	DE TOT	RESULT Q9L3B4 ID Q
LT 2 H2 H2 H2 H3 H4 H3 H4 H5 H5 H5 H6 H7 H7 H7 H7 H7 H7 H7 H7 H7	Query Match 23.4%; Score 34; DB 2; Length 26; Best Local Similarity 50.0%; Pred. No. 2.3e+02; Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 14 SEISVGAEFNKDC 27	SEQUENCE FROM N.A. SEGUENCE FROM N.A. STRAIN-ATCC9937; Felder M., Gupta A., Verma V., Kumar A., Qazi G.N., Cullum J.; Felder M., Gupta A., Verma V., Kumar A., Qazi G.N., Cullum J.; Felder M., Gupta A., Verma V., Kumar A., Qazi G.N., Cullum J.; Felder M., Gupta A., Verma V., Kumar A., Qazi G.N., Cullum J.; "The pyrroloquinoline-quinone synthesis genes of Gluconobacter oxydans."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AJ277117; CAB83197.1; EMBL; AJ277117; CAB83197.1; EMBL; AJ277117; CAB83197.1;	PQQA. Gluconobacter oxydans. Bacteria; Proteobacteria; alpha subdivision; Acetobacteraceae; Gluconobacter. NCBI_TaxID=442;	01-OCT-2000 (TrEMBLrel. 15, Created) 01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-OCT-2000 (TrEMBLrel. 15, Last annotation update) POO PRECURSOR.	LT 1 B4 0913B4 PRELIMINARY; PRT; 26 AA.

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                                                                                      Waterston R.;
Waterston R.;
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U67951; AAB07573.1; -
EMBL; U67951; AAB07573.1; -
SEQUENCE 22 AA; 2535 MW; 35EA30AF96C960B5 CRC64;
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                                                                                                                                                                                                                                                                       Wilson R., Alnscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
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Q94182;
O1-FEB-1997 (Tr
O1-FEB-1997 (Tr
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COSMID C47C12.
C47C12.5;
                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                          STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                     elegans.", Nature 368:32-38(1994).
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STRAIN-BRISTOL N2;
MEDLINE-94150718; PubMed-7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caenorhabditis elegans.
Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDILINE-95345843; PubMed-7620461;
ITATO P., Piccinni E., James P., Ammermann D.;
"Byidence of a cadmium-thionein and the glycine cleav
Oxytricha granulifera.";
Oxytricha granulifera.";
J. Eukaryot. Microbiol. 42:376-378(1995).
SEQUENCE 19 AA; 2381 MW; 4C0B5E62B50A0984 CRC64;
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NCBI_TaxID=5947;
               HLDV--SLAFSEISVGAE
HSDIGNSLQFSRISLKNE 21
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rinae; Caenorhabditis.
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Pred. No. 5.
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Pred. No. 4.7e-
3; Mismatches
                                            Mismatches
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and the glycine cleavage system in
                                       DB 5; L. 5.5e+02; 5;
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4.7e+02;
4;
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                                                                 Length 22;
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                                        Indels
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Best Local :
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nitrosomonas europaea.
Nitrosomonas europaea.
Bacteria; Proteobacteria; beta subdivision;
Ammonia-oxidizing bacteria; Nitrosomonas.
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01-MAY-2000
01-MAY-2000
01-JUN-2001
                                                                                                                                                                                                                                                                                     InterPro; IPR000345; CytC_heme_bind. PROSITE; PS00190; CYTOCHROME_C; UNK
                                                                                                                                                                                                                                                                                                                                          J. Biol. Chem. 268:14645-14654(1993).
HSSP; Q50925; 1FGJ.
                                                                                                                                                                                                                                                                                                                                                                               of an octa-heme subunit."
                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=93315429; PubMed=8325841;
                                                                                                                                                                                                                                                                                                                                                                                   "Hydroxylamine oxidoreductase from Nitrosomonas europaea
                                                                                                                                                                                                                                                                                                                                                                                                                        Arciero D.M., Hooper A.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYDROXYLAMINE OXIDOREDUCTASE (FRAGMENT).
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Q41052;
Q1-NOV-1996
Q1-NOV-1996
Q1-NOV-1998
VAR. AMPLIFO
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EMBL; L26175; AAA72417.1; -.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 08, Last annotation update)
VAR. AMPLIFOLIA DNA SEQUENCE WITH PARTIAL CDS (FRAGMENT).
Porphyra spiralis.
Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae;
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MEDLINE-94224117; PubMed-8170361;
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983D4B8A13698849 CRC64;
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01-NOV-1996
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01-MAY-2000
01-JUN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-95232503; PubMed-7716520; Smith A.B., Esko J.D., Hajduk S.L.; "Killing of trypanosomes by the human haptoglobin-related Science 268:284-286(1995).
        Viruses; Retroid viruses; NCBI_TaxID=11909;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
T-CELL LYMPHOTROPIC VIRUS TYPE 2 TAX (FRAGMENT).
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Eukaryota; E
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                  Human T-cell leukemia virus type II (HTLV-II)
Viruses; Retroid viruses; Retroviridae; Delta
                                                     T-CELL
                                                                                                          Q82410
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Viruses; Retroid viruses; Retroviridae; Delta
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nes 6; Conserv
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-1996 (TrEMBLrel. 01, Last sequence update)
-1998 (TrEMBLrel. 08, Last annotation update)
LYMPHOTROPIC VIRUS TYPE 2 TAX (FRAGMENT).
                                                                                                                                                                                                           Similarity
5; Conserv
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Pred. No. 1
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Pred. No. 1
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annotation update)
SUBUNIT (FRAGMENT)
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                    Deltaretrovirus
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Sches 5; Conservative
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Q1-NOV-1996
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Q82412;
Q1-NOV-1996
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
T-CELL LYMPHOTROPIC VIRUS TYPE 2 TAX (FRAGMENT).
                                                                                  TAX.
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            MEDLINE=96190544;
                      SEQUENCE FROM N.A.
                                                           Viruses;
                                                                      Human
                                                                                            T-CELL
                                                                                                       01-NOV-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human T-cell leukemia virus type II (HTLV-II)
Viruses; Retroid viruses; Retroviridae; Delta
                                             NCBI_TaxID=11909;
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                                                          T-cell leukemia virus type II (HT es; Retroid viruses; Retroviridae;
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                                                                                           -1996 (TIEMBLIEL. 01, Created)
-1996 (TIEMBLIEL. 01, Last sequence update)
-1998 (TIEMBLIEL. 08, Last annotation update)
LYMPHOTROPIC VIRUS TYPE 2 TAX (FRAGMENT).
 Novoa
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           PubMed=8627666;
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Pred. No. 1.5e+03;
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Pred. No. 1
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1.5e+03;
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M.D.,
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RESULT

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40.2 KDA HAPTUGE.
Homo sapiens (Human).
Homo sa
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Best Local S
Matches 5
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Q9UC67;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-UN-2001 (TrEMBLrel. 17, Last annotation update)
40.2 KDA HAPTOGLOBIN BETA-CHAIN HOMOLOG (FRAGMENT).
                     MEDLINE-95364343; PubMed-7637327; Kliffen M., de Jong P.T., Luider T.M.; "Protein analysis of human maculae in maculopathy.";
                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q25867;
Q25867;
01-NOV-1996
01-NOV-1996
01-NOV-1996
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa;
NCBI_TaxID=5833;
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Submitted (NOV-1994)
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NON_TER
SEQUENCE
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EMBL; U32885; AAB04925.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 EISVGAEFNKDDC
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5; Conserv
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73:267-272(1995)
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Pred. No. 2e+0
3; Mismatches
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                                                                                                                                                                                                                Craniata; Vertebrata;
Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation updat
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2e+03;
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l.5e+03;
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STRAIN=85P;
STRAIN=85P;
Suerbaum S., Brauer ...
Gene 0:0-0(0).
Gene 0:0-0(0).
TMBL; Y10747; CAA71736.1; -27
27
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AA; 2917 MW
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FLAGELLIN B
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Bacteria; Proteobacteria; epsilon subdivision;
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Kawamoto M., Minamino N., Matsuo H., Eto
"Identification and hypotensive activity
terminal 20 peptide (PAMP).";
FEBS Lett. 351:35-37(1994).
SEQUENCE 20 AA; 2446 MW; 9604950BAF42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metážoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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LGYHLDVSL-AFSEISVGAEFNKD
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                                                              Similarity 5; Conserv
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(FRAGMENT).
                                                        Conservative
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                                                                          18.3%;
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54.5%;
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                                                      Score 26.5; I
Pred. No. 3.5e
10; Mismatches
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Last sequence update)
Last annotation updat
                                                                                                                                               810C3A9337F0BE18 CRC64;
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Pred. No. 2.1e
2; Mismatches
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SEQUENCE
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MEDLINE-85122694; PubMed-6395893;

Genovese C., Rowe D., Kream B.;

"Construction of DNA sequences complementary to rat alpha 1
2 collagen mRNA and their use in studying the regulation of collagen synthesis by 1,25-dihydroxyvitamin D.";

Biochemistry 23:6210-6216(1984).

EMBL, M12200, AAA40835.1; -
                                                                                                                                                                                                                                                                                                                             Q63076;
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"Cell-type-specific regulation of the retinoic acid
by the orphan nuclear receptor TLX.";

MO1. Cell. Biol. 20:8731-8739(2000).

EMBL; AF220160; AAG35363.1; -

EMBL; AF220160; AAG35363.1; -

InterPro; IPR000345; CYtC_heme_bind.

PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.

SEQUENCE 20 AA; 2261 MW; AA77738B0BE3C482 CRC64;
                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                  01-NOV-1996 (TrembLrel 01, 01-NOV-1996 (TrembLrel 01, 01-JUN-2001 (TrembLrel 17, RAT ALPHA-2 TYPE I COLLAGEN
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01-JUN-2001
                                                                                                                            Pfam;
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2358 MW;
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Rodentia;
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33.3%;
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Pterygota; Neoptera; Ende
Psychodidae; Phlebotomus
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NCBI_TaxID=59273;
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Phlebotomus papatasi.
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Insect Mol. Biol. 6:0-0(1997).
EMBL; U94474; AAD09262.1; -.
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EMBL; U94475; AAD09264.1;
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Insect Mol. Biol. 6:0-0(1997).
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3.3e+03;
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                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-SIVSMB7;
MEDLINE-96171634; PubMed-8574147;
Kraiselburd E.N., Torres J.V.;
"Properties of virus-like particles prinfected human cell clones.";
Cell. Mol. Biol. 41:41-52(1995).
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MEDLINE=98109578; PubMed=9449524;
Kraiselburd E.N., Salaman A., Beltran M., Rivera M.,
Kessler M., Knezevich M., Rodriguez A., Bilska M., M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   092820;
01.NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation updat
                                                                                                       SEQUENCE FROM N.A. STRAIN-SIVSMB7;
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InterPro;
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Q9Q123;
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01-MAY-2000
01-JUN-2001
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Pfam; Pr01560; HCV_NS1; 1.
Coat protein; Envelope protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NON_TER
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NCBI_TaxID=11103;
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8; Conser
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(Trembirel. 13, Last sequence update)
(Trembirel. 17, Last annotation update)
PROTEIN [CONTAINS: ENVELOPE GLYCOPROTEIN]
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Pred. No. 4.1e+03;
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MEDILNE=88283628; PubMed=3396534;
Barbas J.A., Chaix J.C., Steinmetz M., Go
"Differential splicing and alternative po
distinct NCAM transcripts and proteins in
EMBO J. 7:625-632(1988).

EMBL; X07196; CAA30174.1; -.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
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Welnberg A., Holt S.C.;
Welnberg A. Holt S.C.;
"Chemical and biological activities of a protein from Treponema denticola strains.
J. Bacteriol. 173:6935-6947(1991).
SEQUENCE 16 AA; 1640 MW; 3245DE6C11C5
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Bacteria; Spirochaetales;
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EMBL; AF034690; AAC09235.1; -.
Envelope protein
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Sciurognathi;
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No.
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polyadenylation
in the mouse.";
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01-NOV-1996
01-JUN-2001
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"Identification of planarian homeobox sequences indicates antiquity of most Hox/homeotic gene subclasses.";
Proc. Natl. Acad. Sci. U.S.A. 92:7227-7231(1995).
EMBL; L41853; AAB17624.1;
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01-MAY-2000 (TIEMBLIE1 13, Last sequence up
01-JUN-2000 (TIEMBLIE1 14, Last annotation
BILE SALT HYDROLASE A (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=93054334; PubMed=1429446;
Lundeen S.G., Savage D.C.;
"Multiple forms of bile salt hydrolase
100-100.";
                                                                                                      InterPro; IPR001356; Homeobox.
Pfam; PF00046; homeobox; 1.
                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE=95365341; PubMed=7638172;
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Bacteria; Firmicutes;
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01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                         J. Clin. Endocrinol. Metab.
HSSP; PO1033; 1UEA.
InterPro; IPR001820; TIMP.
PROSITE; PS00288; TIMP; 1.
SEQUENCE 25 AA; 2698 MW;
                                                                                                                                                                                                               "Partial purification and amino acid sequence analysis of endometriosis protein-II (ENDO-II) reveals homology with tissue inhibitor of metalloproteinases-1 (TIMP-1).";
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Surewicz K.;
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Rodentia;
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                       Compounds modulating CD59 mediated complement activity, for treatment of, e.g. immunovasculitis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human C9 protein fragment (residues 359-384).
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                                                                                                                                                                                                                                                                                                                                              (BLOO-) BLOOD CENT RES FOUND (OKLA-) OKLAHOMA MEDICAL RES
                                                                                                                                                                                                                                                               PJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-0020393.
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                                                                                                                                                                                                                                                                                                                                                  FOUND
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Best Local :
                  Sequences AAY77154-Y77174 represent novel peptides capable of binding the and activating human fibroblast growth factor receptor (FGFR). The peptides of the invention have amino acid sequences that are unrelated to that of the human FGFR or to those of prior art FGFR-binding the following the first of t
                                                                                                                                                                               Claim 16;
                                                                                                                                                                                               New polypeptide useful as a receptor agonist or antagonist in treating wounds and promoting angiogenic capability, and as a model for designing small molecules with agonist or antagonist activity.
                                                                                                                                                                                                                                                                                                                                                                                                      McConnell SJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                             (CHUS ) CHUGAI PHARM CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fibroblast growth factor receptor; FGFR ligand; activation; phage display library; agonist; antagonist; drug screening; competitive inhibitor; angiogenic; wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-JAN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                          2000-160963/14.
DB; AAZ87257.
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27; Conser
                                                                                                                                                                          Page
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                                                                                                                                                                                                                                                                                                                                                                                              Spinella DG
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Pred. No. 3.4e-17;
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from phage display libraries via
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RESULT
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Best Local S
Matches 7
                                         Novel fusion polypeptide comprising first and second caspase subunit separated by cleavage site not associated in nature with caspase subunit, useful for cloning gene encoding enzymes involved in
                                                                                                      WPI; 2001-290920/30.
                                                                                                                                Cordell B,
                                                                                                                                                                           20-OCT-1999; 99US-0160559.
14-AUG-2000; 2000US-0225564.
                                                                                                                                                        (SCIO-)
                                                                                                                                                                                                               19-OCT-2000; 2000WO-US28941
                                                                                                                                                                                                                                                                                           /note=
Misc-difference 11
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                                                                                                                                                                                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                                                                                                                                  Unidentified
                                                                                                                                                                                                                                                                                                                                                                           Amyloid precursor protein; APP; caspase; beta-secretase; cleavage site; cysteine protease; apoptosis; caspase expression cassette; metastasis; tumour; cathepsin B; urokinase; proliferation; gene therapy; interdomain linker; Alzheimer's disease; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                         pCBC1 APP beta-secretase cleavage site (NL/KI) mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 their ability to bind an FGFR probe. Peptide 13-1 (AAY77161) was used as the basis for the construction of an evolved phage display library, which led to the identification of further peptides (AAY77168-Y77174, consensus sequence AAY77153) capable of binding human FGFR. The peptides as competitive inhibitors to inhibit the binding of FGF to its receptor. human FGF. The peptides are useful as FGFR agonist or antagonist therapeutic agents for treating wounds and promoting angiogenesis. The have FGFR agonist or antagonist activity. The peptides are also useful as a model for designing small molecules which economical, and are alternatives to expensive recombinant FGF or FGF therapeutic addition, they have an improved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE00613;
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50.0%;
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                                                                                                                                                                                                                                                                                   "Wild-type Leu
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Pred.
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The present amino acid Disclosure; Fig 29A;

sequence

is a

PCBC1

plasmid amyloid precursor

116pp;

English.

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RESULT
AAW35697
    Query Match
Best Local
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Sequences AAW35694-99 represent 15-20 residue peptides of white faced hornet antigen 5 molecule. The invention relates to peptides derived from vespid venom antigen 5 (VV5) that are antigenic for T cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to a method for functional cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              interdomain linker replaced by swedish mutant beta-secretase cleavage site. This modified caspase-3 plays a pivotal role in Alzheimer's disease. Caspases are a family of cysteine proteases, that participate in the initiation and execution of apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein (APP) beta-secretase cleavage site (AAE00611) (NL/KI) mutant. APP sequence containing this mutation is less susceptible to beta-secretase sequence to site is used to construct an artificially engineered chimeric cassette comprising human caspase-3 with
                                                                                                                         Vespid venom antigen 5 peptide fragments diagnose vespid venom sensitivity
                                                                                                                                                                                        WPI; 1997-470817/43.
                                                                                                                                                                                                                                                                        (UYRQ ) UNIV ROCKEFELLER
                                                                                                                                                                                                                                                                                                                                                          11-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                            W09733910-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dolichovespula maculata
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                                                                                Example 1; Figure 2; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                   18-SEP-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunomodulatory peptide; vespid antigen 5; immunogenic; allergy;
vespid venom; white face hornet wasp; immunodominant peptide; T cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             maculata
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                                                                                                                                                 useful to
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       proliferation in mice immunised with VV5. The peptides can be used treat or diagnose vespid venom sensitivity e.g. to Dolichovespula maculate (white face hornet), Vespula vulgaris (yellowjacket), V.
       AAW82023-W82240 are peptides used in the construction of a fluorogenic composition which is used for the detection of protease activity in biological samples. The products can be used for the detection of conformation changes in nucleic acids, oligosaccharides,
                                                                                          New fluorogenic compositions - containing 2 fluorophores separated by a peptide comprising a protease binding site, used for detecting protease activity in samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fluorogenic protease indicator
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW82186 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P. fuscatis (paperwasp).
                                                                     Disclosure; Page 28; 90pp; English.
                                                                                                                                          WPI; 1998-467579/40.
                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              conformation
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                                                                                                                                                                                                                                                                                                                                                          /note=
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 proteins,
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                                                                                                                                                                                                                                                                                                                        "epsilon-aminocaproic acid,
                                                                                                                                                                                                                                                                                                                                                           "epsilon-aminocaproic acid,
                                                                                                                                                                                                                                                                                                                                                                                "alpha-aminoisobutyric acid, labelled
amino acid B in the specification"
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peptides
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           detection; fluorogenic; cellular uptake;
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 phopholipids,
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RESULT AAAG7 3203 1D AAAG7 3203 2D AAAG7 3203 2D AAAG7 2XX AAAG7 XXX AAAG7 AAAAG7 AAAG7 AAAG7 AAAG7 AAAG7 AA
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Best Local Similarity 53.5.
Best Local Similarity 53.5.
Conservative
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The present invention describes fluorogenic compositions which can be used for the detection of protease activity. This can be useful as an indicator of viral infection, cancer metastasis, haemophilia, emphysema peptide, a peptide spacer and a donor and an acceptor fluorophore. The detected. The present sequence is one of the peptides can then be exemplification of the invention.
                                                                                                                                                                                                                                                                                                     New fluorogenic compositions whose fluorescence level increases in the presence of active proteases, useful for detecting and localizing protease activity in biological samples, particularly in frozen tissue
                                                                                                                                                                                                                                                         Disclosure; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Komoriya A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-SEP-2000; 2000WO-US24882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ONCO-) ONCOIMMUNIN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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/note≈ "2-aminoisobutyric acid"
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                                                                                                                                                                                                                                                 86pp; English.
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Query Match
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                                                                            The present invention describes fluorogenic compositions which can used for the detection of protease activity. This can be useful as indicator of viral infection, cancer metastasis, haemophilia, emphy heptide, a peptide spacer and a fluorogenic compositions comprise a peptide is cleaved by a protease and the fluorophores can then be detected. The present sequence is one of the peptides described in
                                                                         detected. The present sequence is exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                New fluorogenic compositions whose fluorescence level increases in the presence of active proteases, useful for detecting and localizing protease activity in biological samples, particularly in frozen tissue samples
                                                                                                                                                                   Disclosure;
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8; Conser
                                                                                                                                                              Page 27; 86pp; English.
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/note= "2-aminoisobutyric acid"
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                                                                                              fluorophore. The
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Score 34; DB Pred. No. 74;

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Best Local Similarity
BCl-XL/BCl-2 associated cell death regulator; BAD; mutant; apoptosis;
immunostimulant; neuroprotective; nootropic; antiischaemic; vulnerary;
cytostatic; antiviral; antiarthritic; antiinflammatory; wound healing;
                                                                                                                                                                                                                                                                                                                                                                            Novel polynucleotide encoding a BBC3 protein which is useful for modulating apoptosis, especially in the treatment of cancer and autoimmune diseases - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY96324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY96324 standard; Peptide;
                                        BIK BH3 consensus peptide sequence SEQ ID NO:7.
                                                                                                                                                                                                                                                                                                      domain of a puta
regulator BBC3,
                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-365560/31.
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                                                                                                     AAB70374 standard;
                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                          autoimmune diseases.
                                                                                                                                                                                                                                                                                 nucleic acids and antibodies are suitable for use in promoting cell death or for preventing apoptosis in malignant cells and those causing
                                                                                                                                                                                                                                                                                                      The present sequence is the mammalian Bik Bcl-2 homology domain 3 (BH3) domain, which was used in a sequence alignment with the same domain of a putative version of the mammalian apoptosis regulator BBC3, which was designated BBC3-ORF2. The BBC3 protein,
                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 4; 47pp; English.
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is inhibition;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Chittenden
                                                                                                     Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cell death; BBC3; apoptosis promotion;
on; malignant cell; autoimmune disease.
                                                             entry)
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ID AAB3
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Cytostatic; neuroprotective; cardiant; Bcl-2 superfamily; apoptosis modulation; B cell

lymphoma/leukemia 2; cancer;

prostate;

anti-HIV; virucide; cerebroprotective; BH3 domain; cell death agonist; Bad;

Bcl2 polypeptide BH3 domain peptide #16.

(first

entry)

AAB37016;

AAB37016 standard;

peptide;

27

10

11 cigdemdvsl

0

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Query Match
Best Local Similarity
                                    Matches
                                                                                                                                                                                lymphoproliferative conditions, arthritis, infertility, inflammation and autoimmune diseases. The present sequence represents a Bcl-family member BH3 domain consensus sequence which is used in an example from the
                                                                                                                                                                                                                                 can be used as an apoptosis inducer or inhibitor. BAD polypeptides and polynucleotides can be used for screening candidate compounds and drugs for activity that promote cell survival or apoptosis. Other uses include inducing or inhibiting apoptosis in a cell. Candidate compounds identified and (mutant) BAD polypeptides are useful in treating immunodeficiency diseases, neurodegenerative diseases, ischaemic cell death, reperfusion cell death, wound healing, cancer, viral infections,
                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes an isolated or synthetic polypeptide (I) comprising a less than full length amino acid sequence of a mutant Bcl-XL/Bcl-2 associated cell death regulator polypeptide (BAD) or its fragment, which contains amino acid substitutions at Serll8 of a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                userul for screening apoptosis, comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide, useful for screening for candidate compounds which induce or inhibit apoptosis, comprises amino acid substitutions at Ser118, Ser155 or
                                                                                                                                                                                                                                                                                                                                                                                                          BAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunosuppressive; apoptosis inducer; apoptosis inhibitor; cance immunodeficiency disease; neurodegenerative disease; viral infectischaemic cell death; reperfusion cell death; arthritis; infertilymphoproliferative condition; inflammation; autoimmune disease.
                                                                                                                             Sequence
                                                                                                                                                                 present invention.
                                                                                                                                                                                                                                                                                                                                                                    antiarthritic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-138734/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (APOP-) APOPTOSIS TECHNOLOGY INC
2 CLGYHLDVSL
                                                                                                                                                                                                                                                                                                                                                                , Ser155 of a murine BAD (longer murine BAD) or Ser113 of a murine (shorter murine BAD). (I) has immunostimulant, neuroprotective, tropic, antiischaemic, vulnerary, cytostatic, antiviral, iarthritic, antiinflammatory and immunosuppressive activities, and
                                    6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fig
                                                                                                                              26
                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3a;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0136783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   157pp; English
                                                      23.4%;
                                    2;
                                                     Score 34;
Pred. No.
                                       Mismatches
                                                      96;
                                                                         DВ
                                                                        22;
                                    2;
                                                                      Length
                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           il infection; infertility;
                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             inhibit
                                    Gaps
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RESULT
AAU15328
                                                                                                                                                                                                                                                               CC (R-X)n-peptide where n = 1-10; X = C-0, when the R-X group is attached CC (R-X)n-peptide where n = 1-10; X = C-0, when the R-X group is attached CC to the N-terminus of the peptide, or a side chain of the peptide where CC when the R-X group of the side chain is NH2 or OH; Or X = O OR NH. CC side chain of the peptide, where the side chain functional group is attached to the C-terminus of the peptide, or a CC or CONH2; and R = 2-18C alkyl or alkoxy, 2-14C alkylenyl containing one CC or two double bonds, cyclobutyl, cyclopentyl, cyclopentyl cyclopentyl group is COOH CC monosubstituted with a 1-5C straight or branched chain alkyl group, alkyl group, or benzyl. The peptides AAB37001-B3705 represent examples CC of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of CC useful for modulating apoptosis in the cells of a subject, or for constaining a cells. It is also useful for inhibiting Bcl-2 corresponding to amino acids 72-97 of CC subject afflicted with a cancer characterized by cancer cells that con-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or conjugate is also useful for inhibiting Bcl-2. The cancer includes prostate, colorectal, gastric, coloreased apoptosis, e.g. neurodegenerative disorders, acquired by cancer characterized by cancer cells that con-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or conjugate is also useful for treating a concercased apoptosis, e.g. neurodegenerative disorders, acquired immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
                                                                                                                                                                                                                                                                 Matches
      Schizophrenia-associated isoform peptide #213.
                                        24-OCT-2001
                                                                 AAU15328;
                                                                                  AAU15328 standard; Peptide; 13 AA
                                                                                                                                                  New peptide conjugates for modulating apoptosis or for inhibiting cell lymphoma/leukemia 2 (Bel-2) function, especially useful for treating neurodegenerative disorders, stroke, or cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 18; Page 18; 74pp; English.
                                                                                                                                                                                                  Local Similarity tes 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-679325/66.
                                                                                                                                                                       2 CLGYHLDVSL 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Huang Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma; melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS; stroke; myocardial infarction.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wang J,
                                                                                                                                                                                                Conservative
                                   (first entry)
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                                                                                                                                                                                                         23.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhang Z,
                                                                                                                                                                                           Score 34; DB 21
Pred. No. 1e+02;
2; Mismatches
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The invention relates to methods and compositions for screening, CC diagnosis and prognosis of Schizophrenia. The method involves detecting the presence of Schizophrenia (SCH) Associated Features (SFs) and SCH associated Protein Isoforms (SFIs) in samples, e.g. by electrophoresis, CC studying the effectiveness of treatments and for identifying potential CC Schizophrenia (SCH) and the relative abundance of at least 1 chosen feature correlates (CC therapy administered to a subject with SCH and the relative abundance of at least 1 chosen feature correlates (CC therapy administered to a subject with SCH and the relative abundance of CC at least 1 chosen feature which correlates with the severity of SCH.

CC (e.g. secondary messengers) are studied to diagnose SCH, monitor the CC targets to identify and produce potential therapeutic agents for the CC treatment of SCH. The paucity of detectable neuralyic defects and stinguishes neuropsychiatric disorders such as SCH from neurological converted the interfect of any been identified in many cases. Consequently the identification and CC disorders, where manifestations of anatomical and biochemical changes characterisation of cellular and/or molecular causative defects and consequents. AAUI5162 represent the amino acid sequences of the anatomical invention.
       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Diagnosing and monitoring Schizophrenia by detecting the presence of schizophrenia Associated Features and Schizophrenia Associated Protein Isoforms in samples of cerebrospinal fluid -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-502868/55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-FEB-2000; 2000GB-0004415.
28-NOV-2000; 2000US-0750395.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (OXFO-) OXFORD GLYCOSCIENCES UK LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-FEB-2001; 2001WO-GB00783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W0200163293-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schizophrenia; neuroleptic; diagnostic; neuropsychiatric disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neurological disorder; neuropathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Page 33; 160pp;
13 AA;
                                                 1soforms used in the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rohlff C;
                                         the invention.
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Matches
Schizophrenia-associated isoform peptide #223.
                        24-OCT-2001
                                          AAU15338;
                                                       AAU15338 standard; Peptide;
                                                                                                                    10 SLAFSEISVGAE 21
                                                                             12
                                                                                                  1 sldfteldvaae
                                                                                                                                                   Local
                                                                                                                                        Similarity 7; Conserv
                                                                                                                                      Conservative
                    (first entry)
                                                                                                    12
                                                                                                                                              22.8%;
58.3%;
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                                                                                                                                             Score 33;
Pred. No.
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RESULT 13
AAW38432
ID AAW38
XX AAW38
AC AAW
AC AAW
XX
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XX
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XX
DT 2'
XX
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Best Local Similarity
Thes 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Associated Protein Isoforms (SPIS) in samples, e.g. by electrophoresis, immunoassay or hybridisation assay, for diagnosing and monitoring SCH, studying the effectiveness of treatments and for identifying potential therapeutic agents. The method is used for (1) screening or diagnosis of SCH and the relative abundance of at least 1 chosen feature correlates with the presence or absence of SCH; and (2) monitoring the effect of therapy administered to a subject with SCH and the relative abundance of at least 1 chosen feature which correlates with the severity of SCH. The expression and activity of the SFS, SPIS and related molecules (e.g. secondary messengers) are studied to diagnose SCH, monitor the progress of the disorder and the effectiveness of treatment and as
                                                                                                                                                                                                                                                                                                                                                                                                                                                neuropathies are necessary for improved treatment of neuropsychiatric disorders. AAU15114-AAU15762 represent the amino acid sequences of schizophrenia-associated isoforms used in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    targets to identify and produce potential therapeutic agents for the treatment of SCH. The paucity of detectable neuralgic defects distinguishes neuropsychiatric disorders such as SCH from neurological disorders, where manifestations of anatomical and biochemical changes have been identified in many cases. Consequently the identification and characterisation of cellular and/or molecular causative defects and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Diagnosing and monitoring Schizophrenia by detecting the presence of Schizophrenia Associated Features and Schizophrenia Associated Protein Isoforms in samples of cerebrospinal fluid -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schizophrenia; neuroleptic; diagnostic; neuropsychiatric disorder; neurological disorder; neuropathy.
                                        Human dendritic cell receptor DEC-205 peptide 3 (aa82-96).
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to methods and compositions for screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-502868/55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-FEB-2000; 2000GB-0004415.
28-NOV-2000; 2000US-0750395.
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                                                                                                                                                    AAW38432 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diagnosis and prognosis of Schizophrenia. The method involves detecting the presence of Schizophrenia (SCH) Associated Features (SFs) and SCH
                                                                              21-MAY-1998
                                                                                                                 AAW38432;
                                                                                                                                                                                                                                                                                 10 SLAFSEISVGAE 21
                                                                                                                                                                                                                                              Page 33;
 cell receptor; DEC-205; human; ligand; cell targetting;
                                                                                                                                                                                                                                                                                                                                                                                                                 13 AA;
                                                                                                                                                                                                                                                                                                                       Conservative
                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               160pp; English.
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                                                                                                                                                                                                                                                                                                                                      22.8%;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEC-205 peptide 3 corresponds to amino acids 82-96 of the human characteristic cell receptor DEC-205 (see AAM3843). BALB/c mice have been immunised with DEC-205 peptide 1 (see AAM3843) and DEC-205 peptide 2 (see AAM38431). Spleen cells were subsequently fused with NS-1 myeloma cells. A hybridoma, 2F5, was obtained with produced monoclonal antibody binding to peptide 1 but not to peptide 2 or to control DEC-205 peptide 3. The invention provides isolated human DEC-205, its extracellular domain and equivalent fragments, and polynucleotides encoding these polypeptides. Further provided are ligands (preferably an antibody or antibody binding fragment) that bind to human DEC-205, as well as constructs for use in prophylaxis and therapy that comprise such a ligand, human DEC-205 or an extracellular domain coupled to an antigen capable of inducing a protective immune response in a patient, or to a toxin (e.g. ricin A chain to specifically destroy dendritic cells as part immuneruments of the part of the specifically destroy dendritic cells as part immuneruments.
                             subtilisin-kexin isoenzyme 1; SALLI, subtilisin-kexin isoenzyme 1; SALLI, proBDNF; ant pro-brain-derived neurotrophic factor; proBDNF; ant cytostatic; vasotropic; SKI-1 inhibitor; hypercholativer steatosis; Ras-dependent cancer; restenosis; amvloid protein formation.
                                                                                                             Human; beta-amyloid precursor protein; beta-APP; beta-secretase;
subtilisin-kexin isoenzyme 1; SKI-1;
                                                                                                                                                                                                 03-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human dendritic cell receptor, DEC-205 - useful to develop ligands for isolation and targetted cell delivery of antigen or toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antigen; toxin; immunosuppressive; therapy; prophylaxis; monoclonal antibody.
                                                                                                                                                              Human beta-amyloid precursor protein beta-secretase site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-MAY-1997;
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                                                                                                                                                                                                                                                                   AAB06316 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-MAY-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunosuppressive process).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                        22.8%;
43.8%;
                                                                                                                                                                                                                                                                 peptide;
                                                                                                                                                                                                                                                                   16
                                                                                                                                                                                                                                                                                                                                                                                                                         5
                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 33; Pred. No.
                                                                                             factor; proBDNF; antilipaemic;
                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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72;
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20-OCT-1999; 99US-0160559
14-AUG-2000; 2000US-0225564
                                                                     19-OCT-2000; 2000WO-US28941
                                                                                                                                26-APR-2001
                                                                                                                                                                                                                                                     cysteinė protėase; apoptosis; caspase expression cassette; metastasis; tumour; cathepsin B; urokinase; proliferation; gene therapy; interdomain linker; cleavage site; Alzheimer's disease; mutant; mutein
                                                                                                                                                                                WO200129232-A2
                                                                                                                                                                                                                                  Unidentified
                                                                                                                                                                                                                                                                                                                             Beta-amyloid precursor protein; beta-APP; caspase; beta-secretase;
                                                                                                                                                                                                                                                                                                                                                                                                             Beta-amyloid
                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE00609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE00609 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is the beta-secretase site of human beta-amyloid precursor protein (beta-APP). The sequence may be cleaved by a mammalian subtilase, specifically subtilisin-kexin isoenzyme 1 (SKI-1), a type-1 SKI-1 may be used for monitoring SKI-1 activity, for screening inhibitors fragments of SKI-1 which bind to the SKI-1 activity. Proteic inhibitors of SKI-1 which bind to the SKI-1 catalytic site may be used as include hypercholesterolaemia, high levels of fatty activity. They may be used to treat diseases include hypercholesterolaemia, high levels of fatty acids, lipids or and amvinial prophosphate, liver steatosis, Ras-dependent cancer, restenosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel soluble proteic fragment of subtilisin-kexin isoenzyme for producing a polypeptide useful for treating hypercholesterolemia, listeatosis and amyloidosis, comprises a specific amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 4; Page 51; 119pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-365601/31.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 SEISVGAEFNKD 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15
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les 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 sevnldaefrhd 15
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                                                                                                                                                                                                                                                                                                                                                                                                        precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peptide; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22.8%;
                                                                                                                                                                                                                                                                                                                                                                                  protein beta-secretase cleavage site mutant
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Pred. No.
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. 78;
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PI Cordell B, Li Y;

XX

WPI; 2001-290920/30.

XY

Novel fusion polypeptide comprising first and second caspase subunit separated by cleavage site not associated in nature with caspase proteolytic cleavage.

PT subunit, useful for cloning gene encoding enzymes involved in xX

PT subunit, useful for cloning gene encoding enzymes involved in xX

PT subunit, useful for cloning gene encoding enzymes involved in xX

PT subunit, useful for cloning gene encoding enzymes involved in xX

PS Example 2; Page 26; ll6pp; English.

XX

CC The present sequence is a beta-secretase cleavage site of beta-amyloid construct a chimeric cassette comprising human caspase-3 with interdomain the construct a chimeric cassette comprising human caspase-3 with interdomain that participate in the initiation and execution of apphotosis.

CC The present invention relates to a method for functional cloning of encoding proteins or enzymes involved in proteolytic cleavage pivotal that conding sequence of a proteolytic cleavage expression cassettes comprising encoding two caspases subunits. A fusion polypeptide comprising a first in nature, is useful for cloning gene encoding enzymes involved in proteolytic cleavage. In a second caspase subunit, separated by a cleavage site not associated polypeptide is used to identify a mutant cell line deficient in an cryme of interest and is also useful for diagnosis and suppression of correspression of a polypeptide (e.g. Cathepsin B or urokinase, cased in the tumour cell characterised by cased containing fusion of polypeptide is used in gene therapy.

Sequence 18 AA;
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RESULT 16
AAE00611
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Best Local Similarity
  20-OCT-1999;
14-AUG-2000;
                         19-OCT-2000; 2000WO-US28941.
                                                                W0200129232-A2
                                                                                   Unidentified.
                                                                                                 cysteine protease; apoptosis; caspase expression tumour; cathepsin B; urokinase; proliferation; ge interdomain linker; Alzheimer's disease.
                                                                                                             cysteine protease; a tumour; cathepsin B;
                                                                                                                      Amyloid precursor protein; APP; caspase; beta-secretase; cleavage site;
                                                                                                                                           Amyloid precursor protein (APP) beta-secretase cleavage site
                                                                                                                                                                      02-JUL-2001
                                                                                                                                                                                                       AAE00611 standard; peptide;
                                                                                                                                                                                         AAE00611;
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sevnldaefrhd
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99US-0160559
2000US-0225564
                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                 22.8%;
50.0%;
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Pred. No.
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90;
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                                                                                                        gene therapy;
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                                                                                                               cassette; metastasis;
                                                                                                                                                                                                                                                                                                      Length 18
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RESULT 17
AAY69714
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            encoding proteins or enzymes involved in proteolytic cleavage. The invention is based on the use of caspase expression cassettes comprising the coding sequence of a proteolytic cleavage site flanked by sequences encoding two caspase subunits. A fusion polypeptide comprising a first and a second caspase subunit, separated by a cleavage site not associated in nature, is useful for cloning gene encoding enzymes involved in proteolytic cleavage. An expression cassette containing fusion polypeptide is used to identify a mutant cell line deficient in an enzyme of interest and is also useful for diagnosis and suppression of proliferation or metastases of a tumour cell characterised by selectively expressed in the tumour cells). DNA encoding fusion polypeptide is used in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel fusion polypeptide comprising first and second caspase subunit separated by cleavage site not associated in nature with caspase subunit, useful for cloning gene encoding enzymes involved in proteolytic cleavage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alzheimer's disease. Caspases are a family of cysteine proteases, that participate in the initiation and execution of apoptosis. The present invention relates to a method for functional cloning of generoding proteins or enzymes involved in proteolytic cleavage. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present amino acid sequence is a beta-secretase cleavage site of an amyloid precursor protein (APP). This sequence is used to construct an artificially engineered chimeric cassette comprising human caspasewith interdomain linker replaced by swedish mutant beta-secretase
05-JUN-1998;
31-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                  AAY69714 standard; peptide; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 28A; 116pp; English.
                                                  04-JUN-1999;
                                                                               16-DEC-1999
                                                                                                                WO9964587-A1
                                                                                                                                                Synthetic
                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                Alzheimer's disease
                                                                                                                                                                                                                                Nootropic; neuroprotective; beta-amyloid precursor protein;
                                                                                                                                                                                                                                                               Beta-APP alpha-secretase substrate [NL]-APP(-10,+10).
                                                                                                                                                                                                                                                                                                  11-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cleavage site. This modified caspase-3 plays a pivotal role in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SCIO-) SCIOS INC
                                                                                                                                                                                                                  .eavage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 6; Conserv
                                                                                                                                                                                                                  site; beta-secretase; neurodegenerative disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                (first entry)
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98FR-0007068
99US-0122599
                                                  99WO-FR01326.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22.8%;
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                                                                                                                                                                                                                                                                                                                                                                  A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22;
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                                                                                                                                                                                                                                 metabolism;
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptides AAY69702-Y69718 represent synthetic peptide substrates for a novel polypeptide with beta-secretase activity that can cleave specifically the natural beta-amyloid precursor protein (bAPP). Normal cleavage of the protein occurs between amino acids Met596-Asp597 and val636-Ile637 (positions 4-5 and 44-45 of AAY69701). The novel polypeptide is used to identify agents that interact specifically with it. These agents regulate metabolism of APP, particularly they slow down or reduce production of beta-amyloid, so can be used to treat neurodegenerative diseases, particularly Alzheimer's disease.
                                                                                                             (RHON )
(UYPA-)
                              Polypeptide with beta-secretase activity, specific for wild-type amyloid precursor protein, useful in treating Alzheimer's diseas
                                                                                                                                                                                                                                                       Homo sapiens
Synthetic.
                                                                                                                                                                                                                                                                                                     cleavage
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                                                                                                                                                                                                                                                                                                                                                                                                             AAY69716 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polypeptide with beta-secretase activity, specific for wild-type amyloid precursor protein, useful in treating Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rholam M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (RHON ) RHONE-POULENC RORER (UYPA-) UNIV CURIE PARIS VI
         Example 3;
                                                                  WPI; 2000-097537/08
                                                                                        Rholam
                                                                                                                                                            05-JUN-1998;
                                                                                                                                                                                   04-JUN-1999;
                                                                                                                                                                                                                                 WO9964587-A1
                                                                                                                                                                                                                                                                                                                  Nootropic;
                                                                                                                                                                                                                                                                                                                                        Beta-APP alpha-secretase substrate [NM]-APP(-10,+10).
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6; Conserv
                                                                                                              RHONE-POULENC RORER SA.
UNIV CURIE PARIS VI P & M.
                                                                                                                                                                                                                                                                                                      site; beta-secretase;
                                                                                                                                                                                                                                                                                                      neuroprotective; beta-amyloid precursor protein; metabolism;
ite; beta-secretase; neurodegenerative disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Munoz-Gimenez N,
         Page
                                                                                       Munoz-Gimenez N,
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99US-0122599
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         44pp;
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                                 Alzheimer's disease
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RESULT 1
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PN W09(
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AAW08359-W08362 represent substrates for the enzyme of the invention.

CC The enzyme of the invention is beta-secretase, and specifically cleaves compared to occur via cleavage between residues 16 and 17 of the compared to occur by beta-secretase. Pathogenic processing to beta-app CC beta-amyloid peptide region by an alpha-secretase. Pathogenic processing the invention, which detects at least one of the beta-app CC products formed on cleavage. The method can be used to determine whether compounds effective to at least partially inhibit processing that-app. Compounds effective to at least partially inhibit cleavage of beta-app in cells or mammalian hosts. Isolation and purification of beta-secretase.

CC will permit chemical modelling of a critical event in the pathology of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 뭐
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Best Local
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07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein - us
Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Beta-secretase which specifically cleaves protein - useful to screen for inhibitors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mcconlogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anderson JP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ATHE-) ATHENA NEUROSCIENCES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W09640885-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Beta-cleavage site; beta amyloid precursor protein; APP; beta-secretase; alpha-secretase; proteolytic cleavage; inhibitor; Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Beta-secretase substrate #3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW08361;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        novel polypeptide with beta-secretase activity that can cleave specifically the natural beta-amyloid precursor protein (bAPP). Normal val636-11e637 (positions 4-5 and 44-45 of AAY99701). The novel it. These agents regulate metabolism of APP, particularly they slow down neurodegenerative diseases, particularly Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ĽC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disease
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, Sinha S, Tan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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95US-0480498
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                                                                                                                                                                                                                                                                                                                                                                                                    English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jacobson-croak KL, H;
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Pred. No.
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1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 beta-amyloid precursor useful in treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ω
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AAW82188
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AAW82023-W82240 are peptides used in the construction of a fluorogenic composition which is used for the detection of protease activity in conformation changes in nucleic acids, oligosaccharides, proteins, peptides, lipids, phopholipids, glycolipids, plycoproteins, steroids or polymers. In addition, attachment of a The composition is composed of p = peptide comprising a protease binding attached to the amino terminal amino acid and F2 is attached to the protease, F1, F2 peptides = fluorophores where F1 is carboxyl terminal amino acid and S1, S2 peptides = when present, are peptide spacers where S1, when present, is attached to the amino terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Best Local
                                                                                                                                                     Disclosure; Page 29;
                                                                                                                                                                        protease activity in samples.
                                                                                                                                                                          New fluorogenic compositions - containing 2 fluorophores separated
by a peptide comprising a protease binding site, used for detecting
                                                                                                                                                                                                                      WPI; 1998-467579/40
                                                                                                                                                                                                                                           Komoriya A,
                                                                                                                                                                                                                                                             (ONCO-) ONCOIMMUNIN INC
                                                                                                                                                                                                                                                                                     20-FEB-1997;
                                                                                                                                                                                                                                                                                                          20-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alzheimer's disease.
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| sevnldaefrhd
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 activity; fluorphore;
                                                                                                                                                                                                                                          Packard
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                  90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptide;
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                                                                                                                                                                                                                                                                                                                                                                          "epsilon-aminocaproic acid,
                                                                                                                                                                                                                                                                                                                                                                                                "epsilon-aminocaproic acid, amino acid J in the specif
                                                                                                                                                                                                                                                                                                                                                                                                                             "alpha-aminoisobutyric acid, label amino acid B in the specification
                                                                                                                                                                                                                                                                                                                                                                amino acid J in the specification"
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Pred. No. 1.1e.
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         detection; fluorogenic; cellular uptake;
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3;
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                                                                                                                                                                                                                                                                                                                                                                                               specification"
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RESULT 2
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Best Local Similarity
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                                 Query Match
Best Local Similarity
""" 6; Conserv
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07-JUN-1995;
07-JUN-1995;
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                                                                                                                        Sequences AAY33752-Y33756 are synthetic oligopeptides used for measuring the activity of beta-secretase (AAY33741). Beta-secretase is capable of cleaving beta-amyloid protein precursor (APP) (AAY33742). These synthetic peptides contain the cleavage site of APP. Beta-secretase and APP are used in a method for detecting human beta-secretase cleavage of polypeptides and for identifying beta-secretase inhibitors. Inhibition of beta-secretase activity would be useful for chemical modelling of a critical event in the pathology of Alzheimer's disease. Inhibitors of beta-secretase would be useful for the prevention and treatment of Alzheimer's disease and Down's Syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Beta-secretase; beta-amyloid protein precursor; APP; Down's syndrome; Alzheimer's disease; measure activity; cleavage site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY33755 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                        A method for detecting human beta-secretase cleavage of polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic oligopeptide 5-16'SW
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                                                                                                    Sequence
                                                                                                                                                                                                                                                       Examples;
                                                                                                                                                                                                                                                                                                                                      Anderson JP,
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                                                                                                                                                                                                                                                                                                                                                            (ELAN-) ELAN PHARM INC
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                     14 SEISYGAEFNKD 25
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Н
sevnldaefrhd 12
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                                                                                                                                                                                                                                                                             for identifying beta-secretase inhibitors
                                                                                                                                                                                                                                                     Column 30; 43pp;
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                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                    A۾,
                                                                                                                                                                                                                                                                                                                                       Jacobson-Croak KL,
                                                                                                                                                                                                                                                                                                                                                                                 96US-0659984.
95US-0480498.
95US-0485152.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22.8%;
53.3%;
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50
                                                       .0%;
                                                                   . 88
                                                                                                                                                                                                                                                      English.
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                                            Ψ
                                                      Score 33;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 33; DB 19;
Pred. No. 1.1e+02;
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                                             Mismatches
                                                                                                                                                                                                                                                                                                                                       Sinha
                                                                  DB 20;
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RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes fluorogenic compositions which can be used for the detection of protease activity. This can be useful as an indicator of viral infection, cancer metastasis, haemophilia, emphysema, thrombosis and arthritis. The fluorogenic compositions comprise a peptide, a peptide spacer and a donor and an acceptor fluorophore. The peptide is cleaved by a protease and the fluorophores can then be detected. The present sequence is one of the peptides described in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New fluorogenic compositions whose fluorescence level increases in the presence of active proteases, useful for detecting and localizing protease activity in biological samples, particularly in frozen tissue samples
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                                                        14-AUG-2001
                                                                                                                                                                      AAG73206 standard; Peptide; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 27; 86pp; English.
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                                                                                                             AAG73206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Komoriya A, Packard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-SEP-2000; 2000WO-US24882
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/note= "2-aminoisobutyric
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53.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BS;
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Pred. No. 1.1e+02;
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Best Local :
                                                  Protease detection; peptide cleavage; enzyme activity; fluorogenic; viral infection; cancer metastasis; emphysema; arthritis; thrombosis; haemophilia.
            Modified-site
                                            Synthetic
                                                                                                   Protease indicator compound
                                                                                                                            14-AUG-2001
                                                                                                                                                 AAG73316;
                                                                                                                                                                AAG73316 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                The present invention describes fluorogenic compositions which can used for the detection of protease activity. This can be useful as indicator of viral infection, cancer metastasis, haemophilia, emphy peptide, a peptide spacer and a donor and an acceptor fluorophore. Detected: The present sequence is one of the peptides described in
                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 27; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                            New fluorogenic compositions whose fluorescence level increases in the presence of active proteases, useful for detecting and localizing protease activity in biological samples, particularly in frozen tissue samnles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Komoriya A,
                                                                                                                                                                                                                                14 SEISVGAEFN--KDD
                                                                                                                                                                                                                                                            Local Similarity 53.
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/label= OTHER
                 Location/Qualifiers
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/note= "2-aminoisobutyric acid"
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53.3%;
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                                                                                                   peptide #45.
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Pred. No.
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1.1e+02;
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Best Local S
Matches 8
                                         Synthetic.
                                                        Beta-secretase; isotype; beta-amyloid precursor protein; App; beta-amyloid peptide; beta-AP; Alzheimer's disease; Downs syn HCHWA-D; Swedish mutation; maltose binding protein; MBP.
                                                                                                                                                                            Peptide 5-16'SW,
                                                                                                                                                                                                                         18-JUL-2001
                                                                                                                                                                                                                                                                                                                                                    1265
                                                                                                                                                                                                                                                                          AAB47265;
                                                                                                                                                                                                                                                                                                                  AAB47265 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes fluorogenic compositions which can be used for the detection of protease activity. This can be useful as an indicator of viral infection, cancer metastasis, haemophilia, emphysema, thrombosis and arthritis. The fluorogenic compositions comprise a peptide, a peptide spacer and a donor and an acceptor fluorophore. The present sequence is cleaved by a protease and the fluorophores can then be detected. The present sequence is one of the peptides described in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New fluorogenic compositions whose fluorescence level increases in the presence of active proteases, useful for detecting and localizing protease activity in biological samples, particularly in frozen tissue samples
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                                                                                                                                                         for used in beta-secretase assay.
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Pred. No. 1.1e+02;
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                                                                Downs syndrome; MBP.
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                         The sequences given in AAB47262-67 represent synthetic peptides containing the cleavage sites derived from wild-type beta-amyloid precursor protein (APP). These peptides were used in assays utilising partially purified beta-secretase to identify beta-secretase inhibitors. Beta-secretase is thought to be responsible for the pathogenic processing of APP to form beta amyloid peptide (beta-AP) in beta-AP related conditions, e.g. Alzheimer's disease, Downs syndrome, HCHWA-D etc. Beta-secretase has a molecular weight of 260-300 kp and will bind to wheat germ agglutinin but not to concanavalin A. Beta-secretase will cleave both the wild type and the Swedish mutation of APP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chrysler SMS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel antibody that specifically binds native beta-secretase protein, useful for raising anti-idiotypic antibodies and for detecting or diagnosing pathological conditions related to presence of respective
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                                                                                                                                   Conservative
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Pred. No. 1.1e+02;
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seq length: 27
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   protein search, using sw model
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Query
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  Issued_Patents_AA: *
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Gapop 10.0 ,
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Copyright (c) 1993 - 2000 Comp
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/BCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/backfiles1.pep:*
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1 100%
45 summaries
                     PCT-US94-07043A-1
US-08-614-935-17
US-09-130-287-17
US-09-130-287-17
US-09-236-385A-41
US-08-69-984A-11
US-08-69-531-18
US-08-69-531-18
US-08-611-324-11
US-08-611-324-11
US-08-41-902-11
US-08-41-902-12
US-08-541-902-12
US-08-541-902-12
US-08-24-695A-4
US-08-44-931-7
US-08-440-391-7
US-08-948-833A-7
US-08-948-833A-7
US-08-98-597A-32
US-09-236-385A-37
US-09-236-385A-37
US-09-236-385A-37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search time 16.63 Seconds (without alignments) 36.536 Million cell update
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Sequence 1, Appli
Sequence 17, Appl
Sequence 17, Appl
Sequence 112, Appl
Sequence 113, Appl
Sequence 114, Appl
Sequence 114, Appl
Sequence 114, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 44, Appl
Sequence 44, Appl
Sequence 44, Appl
Sequence 44, Appl
Sequence 47, Appl
Sequence 7, Appl
Sequence 32, Appl
                                                                                                                                                                                                                                                                                                                      Description
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		Sequence 59, Appl	Sequence 15, Appl	Sequence 8, Appli	Sequence 8, Appli	Sequence 67, Appl	Sequence 3, Appli		Sequence 19, Appl	Sequence 219, App	Sequence 25, Appl	Sequence 25, Appl	Sequence 25, Appl	Sequence 4, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 41, Appl

ALIGNMENTS

RESULT 1 PCT-US94-07043A-1 PCT-US94-07043A-1 Sequence 1, Application PC/TUS9407043A GENERAL INFORMATION: APPLICANT: Tamburini, Paul P.; Benz, G nter; H bich, APPLICANT: Timburini, Paul P.; Benz, G nter; H bich, APPLICANT: Dieter; Dreyer, Robert N.; Koenig, Gerhar TITLE OF INVENTION: CATHEPSIN D IS AN AMYLOIDOGENIC TITLE OF INVENTION: PROTEASE IN ALZHEIMER S DISEASE COUNTRY: USA ZIP: 06516 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.50 COMPUTER: Sharp PC 4600 OPERATING SYSTEM: MS-DOS SOFTWARE: WordPerfect 5.1 CURRENT APPLICATION DATA: TELEFAX: (203) 937-2795 INFORMATION FOR SEQ ID NO: 1: REGISTRATION NUMBER: 31,060 REFERENCE/DOCKET NUMBER: MTI TELECOMMUNICATION INFORMATION: TELEPHONE: (203) 937-2340 FILING DATE: December 16, 1992 PRIOR APPLICATION DATA: APPLICATION NUMBER: 07/880,914 FILING DATE: May 11, 1992 ATTORNEY/AGENT INFORMATION: NAME: Pamela A. Simonton FILING DATE: November 12, 1993 PRIOR APPLICATION DATA: APPLICATION NUMBER: 07/995,660 CLASSIFICATION: PRIOR APPLICATION NUMBER: PCT/US93/10889 SEQUENCE CHARACTERISTICS: ADDRESSEE: Miles Inc. ADDRESSEE: Miles STREET: 400 Morgan CITY: West Haven STATE: Connecticu NUMBER OF SEQUENCES: LENGTH: TYPE: a APPLICATION NUMBER: FILING DATE: June 2 amino acid Connecticut 400 Morgan Lane 16 amino acids UMBER: PCT/US94/07043A June 21, 1994 3.50 inch, 800 kb storage 224.3

US-08-614-935-17

Sequence 17 Patent No.

Вb

14 SEISVGAEFNKDD 26 Local Similarity 53.8 nes 7; Conservative

53.8%;

2;

Pred. No. 4.1; 2; Mismatches

4.

Indels

SEVKMDAEFRHDD 14

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Sequence 17, Application US/09130287
Patent No. 6106844
GENERAL INFORMATION:
APPLICANT: King, Te P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION UNMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                **REFAL INFORMATION: APPLICANT: King, Te P.

APPLICANT: King, Te P.

TITLE OF INVENTION: IMMUNOMODULATORY PEPTIES OF VESTAL

TITLE OF INVENTION: ANTIGEN 5

NUMBER OF SEQUENCES: 81

CORRESPONDENCE ADDRESS:

ADDRESSE: David A. Jackson, Esq.

ADDRESSE: """ "" kensack Ave, Continental Plaza, 4th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA;
APPLICATION NUMBER: US/08/614,935
FILING DATE: 11-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17, Application US/08614935
o. 5804201
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HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE:

US-09-130-287-17
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Best Local Similarity
Thes 5; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 41, Application US/09236385A Patent No. 6221615
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy dis
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APPLICATION NUMBER: US 08,
FILING DATE: 11-MAR-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/130,287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 EFNKDDC 27
SOFTWARE: Patentin Release #1.0, VGCURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/236,385A
FILING DATE: 25-Jan-1999
                                                                                                     ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TYPE: amino acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                       LUTZ, ROBERT J.
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH MODULATE APOPTOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: CHITTENDEN, Thomas D.; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Hackensack
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
STREET: 4
                                                                                                                                                                                                                                                             STREET: 1455 Peni
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                          ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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411 Hackensack Ave, Continental Plaza, 4th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SS: single
linear
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71.4%;
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Pred. No.
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                                                                                   Version #1.25
                                                                                                                                                                                                                                                                                                                Z.W
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RESULT 3 US-09-130-287-17

APPLICANT: King, Te P.
TITLE OF INVENTION: IMMUNOMODE
TITLE OF INVENTION: ANTIGEN 5
NUMBER OF SEQUENCES: 81

CORRESPONDENCE ADDRESS

DЪ Q

ų

DFNHDDC 11

Matches

Conservative

23.4%;

21 EFNKDDC 27

Query Match
Best Local Similarity

SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide HYPOTHETICAL: NO ANTI-SENSE: NO

FRAGMENT TYPE:

internal

TELEFAX: 201-343-1684 INFORMATION FOR SEQ ID NO:

TELEPHONE: 201-40.
TELEPHONE: 201-343-1684
TELEPHONE: TO ID NO:

201-487-5800

ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy

Floppy disk

COUNTRY: STATE:

USA

Hackensack : New Jersey

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 112, Application US/08802981 Patent No. 6037137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                        TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8400
TELEFAX: 202-942-8484
INFORMATION FOR SEQ ID NO: 41
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: HUNTEY, TOM
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 016865-000300US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Compositions for the Detection of Enzyme TITLE OF INVENTION: Activity in Biological Samples and Methods of Use Thereof
                                                                                   FEATURE:
                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Packard, TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 20-FEI CLASSIFICATION: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 CIGDEMDVSL 20
                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 60.1es 6; Conservative
NAME/KEY:
                              OTHER INFORMATION: /product= "Aib"
                                                NAME/KEY: Modified-site LOCATION: 3
                                                                                                                     STRANDEDNESS:
TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION: NAME: WIXON, HENRY N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             San Francisco
                                                                                                                                                      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 32,073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Townsend and Townsend and Crew LLP Two Embarcadero Center, Eighth Floor
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 Modified-site
                                                                                                                     linear
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N: 435
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Pred. No.
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US-08-659-984A-18
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                                                                                                       US-08-659-984A-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 23.4%;
Best Local Similarity 53.3%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 18, Application US/08659984A Patent No. 5942400
                               Matches
                                               Best
                                                          Query Match
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APPLICANT: Anders
                                                                                                                                                                                                               TELEFAX: 415-326-2422 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 07-JUN-1996
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,152
                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Ve CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/659,984A FILING DATE: 07-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Ctr., 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
                                                                                                                                                                                                                                                                                                                      FILING DATE: 07-JUN-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                              Local Similarity
nes 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                    STRANDEDNESS: sin
TOPOLOGY: linear
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 14 SEISVGAEFNKD 25
                                                                                                                                                                                                                                          TELEPHONE:
                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                           NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94111-3834
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                                                                                                                                                                 amino acid
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Sinha, Sukanto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jacobson-Croak, Kirsten L.
VENTION: Assays for Detecting Beta-Secretase
VENTION: Inhibition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                               Conservative
                                                                                                                     peptide
                                                                                                                                                    single
                                              22.8%;
50.0%;
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                                              Score 33; DE
Pred. No. 39;
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                               Mismatches
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27;
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                                                            Length 21;
                               Indels
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                               Gaps
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1 SEVNLDAEFRHD 12

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RESULT 8
US-08-802-981-114
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Best Local Similarity
"---hes 8; Conserve
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                                                                            Sequence 114, Application US/08802981 Patent No. 6037137
                  GENERAL INFORMATION:
'APPLICANT: Komoriya, Akira
APPLICANT: Packard, Beverly
TITLE OF INVENTION: Composi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-802-981-113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (415) 576-0300
NFORMATION FOR SEQ ID NO: 1
                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION DATA:
APPLICATION NUMBER: US/08/802,981
FILING DATE: 20-FEB-1997
CLASSIFICATION: 435
                                                                                                                                                                     14 SEISVGAEFN--KDD 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                      OLECULE TYPE:
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: Townsend and
                                                                                                                                                           9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Komoriya, Akira
APPLICANT: Packard, Beverly S.
                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: Modified-site LOCATION: 3
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CITY: San Francisco
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Compositions for the Detection
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53.3%;
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Activity in Biological Samples and Methods of Use Thereof
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Pred. No. 39;
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        of Enzyme
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US-08-660-531-18
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                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
""" 8; Conserva
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                                                                                                                                                                       Sequence 18,
Patent No. 6
                                                                                                                                                       GENERAL INFORMATION:
                                                                                                          APPLICANT: Chrysler, Susanna M.S
APPLICANT: Sinha, Sukanto
APPLICANT: Keim, Pamela S.
                                                           CORRESPONDENCE ADDRESS:
                                                                                                       APPLICANT:
                                                                            NUMBER OF SEQUENCES:
                                                                                         TITLE OF INVENTION:
  ADDRESSEE: Townsend and Townsend and Cr
STREET: Two Embarcadero Ctr., 8th Floor
CITY: San Francisco
STATE: California
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COUNTRY:
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LOCATION:
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NUMBER OF SEQUENCES:
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                                                                     Anderson, Jonn . .
WPNTION: Beta-Secretase
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Townsend and Crew LLP

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TELEFAX: (415)
INFORMATION FOR SEQ ID NO: 11
SEQUENCE CHARACTERISTICS:
TENGTH: 21 amino acids
                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
                        14 SEISVGAEFN--KDD 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                    OTHER INFORMATION: /product= "Acp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
                                                                                                                                                                                             OTHER INFORMATION: /product= "Acp"
                                                                                                                                                                                                                                                       OTHER INFORMATION: /product=
                                                                                                                                                                                                                              NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                NAME/KEY: Modified-site LOCATION: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 20-FEE CLASSIFICATION: 435
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OPERATING SYSTEM:
SEVKMDAEFGXPKDD
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                                                        Conservative
                                                                                                                                                                       Modified-site
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SYSTEM: PC-DOS/MS-DOS
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ON: 435
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                                                                   22.8%;
53.3%;
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                                               Score 33; DB 3;
Pred. No. 39;
2; Mismatches
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                                                                           Length 21;
                                               Indels
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US-08-313-200-8
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/480,498
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REGISTRATION NUMBER: 15270-0022
TELECHMUNICATION INFORMATION:
TELECHNOE: 415-326-2400
TELECHNOE: 415-326-2422
                                            APPLICATION NUMBER: US/08/313,200
FILING DATE: 08 NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KONSKI, Antoinette F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 20344-20658.20
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1815-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:

APPLICANT: Baker, James R.

APPLICANT: Koenig, Ronald J.

APPLICANT: Koenig, Ronald J.

TITLE OF INVENTION: THYROID PEROXIDASE EPITOPIC REGIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                ZIP: 94304-1018

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
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CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: si
                                 TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 SEISVGAEFNKD 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
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                             (415) 494-0792
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Pred. No.
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                               Matches
                                             Query Match
Best Local
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Best Local :
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                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERRNCE/DOCKET NUMBER: 44-9
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303-499-8080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                           TELEFAX: 303-499-8089 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/141,324
FILLING DATE: 21-OCT-1993
CLASSIFICATION: 424
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                    MOLECULL N
HYPOTHETICAL: N
                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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                              Local Similarity
les 6; Conserv
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CITY: Boulder
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14 SEISYGAEFNKD 25
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linear
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Pike, Robert N.
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Barr, Philip J.
                              Conservative
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                                             22.1%;
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Pred. No.
                                                                                                                                                                                                                                                                                                          44-93
                                             Score 32; DE
Pred. No. 79;
                               Mismatches
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                                                            DB 1;
                                                            Length 27;
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US-08-541-902-11
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                                                                                                                                                         Sequence 11 Patent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 303-499-8089
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                               Matches
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Best Local
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                                                                                                                                         GENERAL INFORMATION:
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OPERATING SYSTEM: PC_DOS/MS_DOS
SOFTWARE: Patentin Release #1.0, V.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/141,324
FILING DATE: 21-OCT-1993
CLASSIFICATION: 424
ATTORNEY/AGENT ...
APPLICANT: Potempa, Jan S.
APPLICANT: Barr, Philip J.
APPLICANT: Pavloff, Nadine
APPLICANT: Pike, Robert N.
TITLE OF INVENTION: Lysine-specific Porphyromonas gingivalis
TITLE OF INVENTION: Protease
NUMBER OF SEQUENCES: 28
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Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 44-9
TELEPHONE: 303-499-8080
                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Travis, James
APPLICANT: Potempa, Jan S.
APPLICANT: Barr, Philip J.
APPLICANT: Pavloff, Nadine
APPLICANT: Pike, Robert N.
                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Lysine-specific Porphyromonas gingivalis
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee and Winner, P.C.
STREET: 5370 Manhattan Circle, Suite 201
                                                                                                                                                                                                                                                                           14 SEISVGAEFNKD 25
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linear
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NO
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50.0%;
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; Pred. No. 79;
2; Mismatches
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GENERAL INFORMATION:
APPLICANT: Travis, James
APPLICANT: Potempa, Jan S.
APPLICANT: Barr, Philip J.
APPLICANT: Pavloff, Nadine
APPLICANT: Pike, Robert N.
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US-08-541-902-11
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Patent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 303-499-80
TELEFAX: 303-499-8089
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                 TITLE OF INVENTION: Lysine-spring of INVENTION: Protease NUMBER OF SEQUENCES: 28
                                                                                                              COUNTRY: U
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HYPOTHETICAL:
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LENGTH: 27 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33.878
REFERENCE/DOCKET NUMBER: 44
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303-499-8080
   APPLICATION NUMBER:
                                                                                                                                             CITY: Boulder
STATE: CO
                                                                                                                                                      ADDRESSEE: Greenlee and without 5. STREET: 5370 Manhattan Circle, Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 21-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Ferber, Donna M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
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MEDIUM TYPE: Floppy disk
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nes 6; Conserv
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TTY: Boulder
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Greenlee and Winner, P.C. STREET: 5370 Manhattan Circle, Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NO NO
                                                                                                                                                                                                                                     Lysine-specific Porphyromonas gingivalis
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50.0%;
US/08/541,902
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Pred. No. 79;
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: CLASSIFICATION:

US/08/141,324

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RESULT 15
US-08-324-301-3
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Patent No. 5597569
GENERAL INFORMATION:
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Best Local
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ATTORNEY/AGENT INFORMATION:
NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 44-9
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303-499-8080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 303-499-801
TELEFAX: 303-499-8089
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: F
HYPOTHETICAL: NO
                  TELEFAX: 206-727-3601
NFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/141,891
FILING DATE: 25-0CT-1993
ATTORNEY/AGENT INFORMATION:
NAME: POOT, Brian W.
REGISTRATION NUMBER: 32,928
REFERENCE/DOCKET NUMBER: 0N0109A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Marquardt, Hans
TITLE OF INVENTION: A NEW RIBOSOME-INACTIVATING PROTEIN
TITLE OF INVENTION: ISOLATED FROM THE PLANT BRYONICA DIOICA
NUMBER OF SEQUENCES: 27
                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 206-728-4800
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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nes 6; Conserv
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 424
                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 SEISVGAEFNKD 25
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                                                                                                                                                                                                                                                                                                                                                                                                            Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                               3005 First Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Siegall, Clay B.
Gawlak, Susan L.
                                                                                                                                                                                                                                                                                                                                                                                               USA
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NO
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50.0%;
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RESULT 17 US-08-924-695A-44

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Sequence 44, Application US/08924695A Patent No. 5998583

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                                         Query Match
Best Local Similarity
Thes 5; Conserve
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TISSUE TYPE:
US-08-324-301-3
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                                                                                                                             US-08-706-741B-44
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local 9
                                                                                                                                                                                                                            TELEFAX: (314) 727-60 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Bryonica dioica
                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 96;
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION: NAME: HOLLAND, DONALD R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: KORSMEYER, STANLEY J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 77
                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/0 FILING DATE: 09-SEP-1996 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity hes 6; Conserv
                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
5 CIGDEMDVS 13
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                          2 CLGYHLDVS 10
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                                                                                                                                                                                  amino acid
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7733 FORSYTH BLVD., SUITE 1400
                                                                                                                                                                                                                                           (314) 727-6092
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                                                                                                                                                         linear
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                                                                                                                                         peptide
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                                                                      20.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21.4%;
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                                                                    Score 30; DB Pred. No. 67;
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Pred. No. 74;
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                                                                                   DB 2;
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Gaps

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,391
FILING DATE: 12-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7, Application US/08440391
Patent No. 5656725
                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 1455 Pennsylvania Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 9717
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
                                                                                                                                                                                                                                                                                    APPLICANT: CHITTENDEN, Thomas D.; and APPLICANT: LUTZ, Robert J.
TITLE OF INVENTION: MOVEL PEPTIDES AND COMPOSITIONS WHICH
TITLE OF INVENTION: MODULATE APOPTOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
                                                                                                                                                                                         STATE: D.C.
ZIP: 20004
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MOLECULE TYPE:
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APPLICATION NUMBER: US/08/924,695A
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/0
FILING DATE: 09-SEP-1997
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STREET: 7733 FORSYTH BLVD., SUITE 1400
                                                                                                                                                                                                                 Washington
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Pred. No. 67;
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                                                                     Query Match
Best Local Similarity
Matches 5; Conserv
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US-08-440-391-32
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                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/440,391
FILING DATE: 12-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
REFERENCE/DOCKET NUMBER: 104322.147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-440-391-7
                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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Best Local Similarity 55.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 202-942-8484
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: CHITTENDEN, Thomas D.; and APPLICANT: LUTZ, Robert J. APPLICANT: LUTZ, ROBERT J. TITLE OF INVENTION: MOVEL PEPTIDES AND COMPOSITIONS WHICH TITLE OF INVENTION: MODULATE APOPTOSIS UNMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS: 34
CORRESPONDENCE ADDRESS: 34
                                                                                                                                                                                         TYPE: ami
        7 CIGDEMDVS 15
                                      2 CLGYHLDVS 10
                                                                                                                                                                                                                                                                       TELEPHONE: 202-942-8400
TELEFAX: 202-942-8484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 32,073
REFERENCE/DOCKET NUMBER: 10.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Washington
STATE: D.C.
ZIP: 20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                                                       amino acid
)GY: linear
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                                                                                         20.7%;
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                                                                Score 30; DB:
Pred. No. 80;
2; Mismatches
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Pred. No. 80;
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US-08-440-391-7

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Matches Query Match

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                                                                                                                                                                                                                                                                                               Sequence 7, Application US/08908597A Patent No. 5863795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 152, Application US/08248839C
                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: CHITTENDEN, Thomas D.; and
APPLICANT: LUTZ, ROBERT J.
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
TITLE OF INVENTION: MODULATE APOPTOSIS
NUMBER OF SEQUENCES: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 212-878-9655 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Gregg, Valeta A.
REGISTRATION NUMBER: 35,127
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: A Gene Expression System NUMBER OF SEQUENCES: 185
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 36 TELECOMMUNICATION INFORMATION: TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: McConnell, David APPLICANT: Devine, Kevin APPLICANT: O'Kane, Charles
                                                                                                                                                                           CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                        STATE: U. 20004
                                                                                                                 STREET: 1455 re...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 25-MAY CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
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                                                                                                                                                          ADDRESSEE:
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1455 Pennsylvania Avenue, N.W.
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46.2%;
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Pred. No.
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RESULT 22
US-08-908-597A-32
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 32, Application US/08908597A Patent No. 5863795
GENERAL INFORMATION:
                                                                                                               CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US/08/440,391
FILING DATE: 12-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
REGISTRATION INFORMATION:
TELEPHONE: 202-942.84400
TELEPHONE: 202-942.84400
                                                                                  TELEFAX: 202-942-8484 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                         ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/440,391
FILING DATE: 12-MAY-1995
                                             SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: CHITTENDEN, Thomas D.; and APPLICANT: LUTZ, ROBERT J.
TITLE OF INVENTION: MOVEL PEPTIDES AND COMPOSITIONS WHICH TITLE OF INVENTION: MODULATE APOPTOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: 20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 202-942-8484
                                                                                  TELEPHONE: ZUZ TELEPHONE: ZUZ TELEPHONE: ZUZ TENENX: 202-942-8484
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CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE:
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                                TYPE:
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                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
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)GY: linear
                             amino acid
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              linear
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55.6%;
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Pred. No.
                                                                                                                                                      104322.147
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US-08-908-597A-32

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RESULT 24
US-09-236-385A-32
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Best Local Similarity
5; Conserv
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-236-385A-7
                                                     Sequence 32, Application US/09236385A
Patent No. 6221615
GENERAL INFORMATION:
APPLICANT: CHITTENDEN, Thomas D.; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 23
US-09-236-385A-7
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Best Local Similarity
"hehes 5; Conserv
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8400
TELEFAX: 202-942-8484
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Vers
APPLICATION DATA:
APPLICATION NUMBER: US/09/236,385A
FILING DATE: 25-Jan-1999
CLASSIFICATION: CURknown>
NAME: WIXON, HENRY N.
DECTERMENT NICHTERRY N.
TITLE OF INVENTION: MOVEL PEPTIDES AND COMPOSITIONS WHICH MODULATE APOPTOSIS
                                                                                                                                                                               2 CLGYHLDVS 10
                                                                                                                                                                 CIGDEMDVS 15
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: CHITTENDEN, Thomas D.; and
                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                      LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                           NEY/AGENI INCLUDE NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
(C) AT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Washington
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STREET: 1455 Pennsylvania Avenue, N.W.
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                                                                                                                                                                                                             Conservative
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Pred. No. 80;
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Pred. No. 80;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
RAPPLICATION DATA:
APPLICATION NUMBER: PCT/US96/06122
FILING DATE: HEREWITH
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/440,391
FILING DATE: 12-MAY-1995
CLASSIFICATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCT-US96-06122-7
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Best Local Similarity
"atches 5; Conserv:
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7, Application PC/TUS9606122
GENERAL INFORMATION:
APPLICANT: IMMUNOGEN, INC.
TITLE OF INVENTION: MOVEL PEPTIDES AND COMPOSITIONS
TITLE OF INVENTION: WHICH MODULATE APOPTOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-236-385A-32
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
REFERENCE/DOCKET NUMBER: 104
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                          STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                 STREET: 1400
CITY: Washington
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TELEPHONE: 202-942-8400
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 32:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/236,385A
FILING DATE: 25-Jan-1999
ATTORICATION: <UNKnown>
ATTORICATION: <UNKnown>
NAME: WIXON, HENRY N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER REALABLE FORM.

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PATENTIA Release #1.0, Version #1.25
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ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
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1455 Pennsylvania Avenue, N.W.
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             104322.147PCT
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Pred. No. 80;
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TELEPHONE: 202-942-8400
TELEPAX: 202-942-8484
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US96-06122-7
                                                                                                В
                                                                                                                             Qy
Search completed: January 6, 2002, 09:13:06 Job time: 424 sec
                                                                                                                                                                    Query Match 20.7%; Score 30; DB 5; Length 15; Best Local Similarity 55.6%; Pred. No. 80; Matches 5; Conservative 2; Mismatches 2; Indels
                                                                                          2 CLGYHLDVS 10
|:| :|||
7 CIGDEMDVS 15
                                                                                                                                                                  0; Gaps
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